

701049\_sequence\_listing.txt  
SEQUENCE LISTING

<110> Yamanaka, Shinya  
Dainippon Sumitomo Pharma Co., Ltd.

<120> Screening method for somatic cell nuclear reprogramming substance

<130> 701049

<150> JP 2004-042337

<151> 2004-02-19

<150> JP 2004-232961

<151> 2004-08-10

<150> JP 2004-276572

<151> 2004-09-24

<160> 50

<170> PatentIn Ver. 2.1

<210> 1

<211> 1623

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (50)..(1369)

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Leu Lys Arg Phe Gln Thr Leu Val Pro Leu Asp His Lys Gln Gly Thr  
5 10 15

tta ttt gaa att att gga gag ccc aag ttg ccc aag tgg ttc cat gtc 154  
Leu Phe Glu Ile Ile Gly Glu Pro Lys Leu Pro Lys Trp Phe His Val  
20 25 30 35

gaa tgc ctg gaa gat cca aaa aga ctg tac gtg gaa cct cgg cta ctg 202  
Glu Cys Leu Glu Asp Pro Lys Arg Leu Tyr Val Glu Pro Arg Leu Leu  
40 45 50

gaa atc atg ttt ggt aag gat gga gag cac atc cca cat ctt gaa tct 250  
Glu Ile Met Phe Gly Lys Asp Gly Glu His Ile Pro His Leu Glu Ser  
55 60 65

atg ttg cac acc ctg ata cat gtg aac gtg tgg ggc cct gaa agg cga 298  
Met Leu His Thr Leu Ile His Val Asn Val Trp Gly Pro Glu Arg Arg  
70 75 80

gct gag att tgg ata ttc gga ccg ccg cct ttc cga agg gac gtt gac 346  
Ala Glu Ile Trp Ile Phe Gly Pro Pro Pro Phe Arg Arg Asp Val Asp  
85 90 95

cgg atg ctc act gat ctg gct cac tat tgc cgc atg aaa ctg atg gaa 394  
Arg Met Leu Thr Asp Leu Ala His Tyr Cys Arg Met Lys Leu Met Glu  
100 105 110 115

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ata Ile	gag Glu	gct Ala	ctg Leu	gag Glu 120	gct Ala	gga Gly	gtt Val	gag Glu	cgt Arg 125	cgt Arg	cgt Arg	atg Met	gcg Ala	gcc Ala 130	cat His	442
aag Lys	gct Ala	gcc Ala	acc Thr 135	cag Gln	cct Pro	gct Ala	ccc Pro	gtg Val 140	aag Lys	gtc Val	cgc Arg	gag Glu	gct Ala 145	gcc Ala	cct Pro	490
cgg Arg	ccc Pro	gct Ala 150	tcc Ser	gtg Val	aag Lys	gtc Val	cct Pro 155	gag Glu	acg Thr	gcc Ala	acc Thr	cag Gln 160	cct Pro	gct Ala	ccc Pro	538
gtg Val	aag Lys 165	gtc Val	cgc Arg	gag Glu	gct Ala	gcc Ala 170	cct Pro	cag Gln	ccc Pro	gct Ala	ccg Pro 175	gtg Val	cag Gln	gag Glu	gtc Val	586
cgc Arg 180	gag Glu	gct Ala	gcc Ala	cct Pro	cag Gln 185	cag Gln	gct Ala	tcc Ser	gtg Val	cag Gln 190	gag Glu	gag Glu	gtc Val	cgc Arg	gag Glu 195	634
gct Ala	gcc Ala	acc Thr	gag Glu	cag Gln 200	gct Ala	ccc Pro	gtg Val	cag Gln	gag Glu 205	gtc Val	cgc Arg	gag Glu	gct Ala	gcc Ala 210	acc Thr	682
gag Glu	cag Gln	gct Ala	ccc Pro 215	gtg Val	cag Gln	gag Glu	gtc Val	agc Ser 220	gag Glu	gct Ala	gcc Ala	acc Thr	gag Glu 225	cag Gln	gct Ala	730
ccc Pro	gtg Val	cag Gln 230	gag Glu	gtc Val	aac Asn	gag Glu	gct Ala 235	gcc Ala	acc Thr	gag Glu	cag Gln	gct Ala 240	tcc Ser	gtg Val	cag Gln	778
gcg Ala	gtc Val 245	cgc Arg	gag Glu	gct Ala	gcc Ala	acc Thr 250	cgg Arg	ccg Pro	gct Ala	ccc Pro	ggg Gly 255	aag Lys	gtc Val	cgc Arg	aag Lys	826
gcg Ala 260	gcc Ala	acc Thr	cag Gln	ccg Pro	gct Ala 265	ccg Pro	gtg Val	cag Gln	gtt Val	tgc Cys 270	cag Gln	gag Glu	gcc Ala	acc Thr	cag Gln 275	874
ttg Leu	gct Ala	ccc Pro	gtg Val	aag Lys 280	gtc Val	cgc Arg	gag Glu	gcg Ala	gcc Ala 285	acc Thr	cag Gln	ccg Pro	gct Ala	tcc Ser 290	ggg Gly	922
aag Lys	gtc Val	cgc Arg	gag Glu 295	gcg Ala	gcc Ala	acc Thr	cag Gln	ttg Leu 300	gct Ala	cct Pro	gtg Val	aag Lys	gtc Val 305	cgc Arg	aag Lys	970
gca Ala	gcc Ala	acc Thr 310	cag Gln	ttg Leu	gct Ala	cct Pro	gtg Val 315	aag Lys	gtc Val	cac His	gag Glu	gcg Ala 320	gcc Ala	acc Thr	cag Gln	1018
ccg Pro	gct Ala 325	ccg Pro	ggg Gly	aag Lys	gtc Val	agc Ser 330	gat Asp	gct Ala	gcc Ala	acg Thr	cag Gln 335	tcg Ser	gct Ala	tcg Ser	gtg Val	1066
cag Gln 340	gtt Val	cgt Arg	gag Glu	gct Ala	gcc Ala 345	acg Thr	cag Gln	ctg Leu	tct Ser	ccc Pro 350	gtg Val	gag Glu	gcc Ala	act Thr	gat Asp 355	1114
act Thr	agc Ser	cag Gln	ttg Leu	gct Ala	cag Gln	gtg Val	aag Lys	gct Ala	gat Asp	gaa Glu	gcc Ala	ttt Phe	gcc Ala	cag Gln	cac His	1162

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360

365

370

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act tca ggg gag gcc cac cag gtt gcc aat ggg cag tct ccc att gaa 1210
Thr Ser Gly Glu Ala His Gln Val Ala Asn Gly Gln Ser Pro Ile Glu
375 380 385

gtc tgt gag act gcc acc ggg cag cat tct cta gat gtc tct agg gcc 1258
Val Cys Glu Thr Ala Thr Gly Gln His Ser Leu Asp Val Ser Arg Ala
390 395 400

ttg tcc cag aag tgt cct gag gtt ttt gag tgg gag acc cag agt tgt 1306
Leu Ser Gln Lys Cys Pro Glu Val Phe Glu Trp Glu Thr Gln Ser Cys
405 410 415

ttg gat ggc agc tat gtc ata gtt cag cct cca agg gat gcc tgg gaa 1354
Leu Asp Gly Ser Tyr Val Ile Val Gln Pro Pro Arg Asp Ala Trp Glu
420 425 430 435

tca ttt atc ata tta taaatgcatc tctggtgtga gccaggatag atggtacacg 1409
Ser Phe Ile Ile Leu
440

tctgcaaatc cagaacctaa aggcaggggt tagcttgggc tgagtaaggc aatgatctta 1469
aacctcagcc tgcctaagac tcccttcacatc tttctttctg gtttttgccc taggaatcgg 1529
gaagaacaga gtagagctgt ttttgtttcc ccattgtggt aaatgtttgc agacacaatt 1589
taaagtattc taataaaaaa aaaattgcat tccc 1623

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<210> 2  
 <211> 440  
 <212> PRT  
 <213> Mus musculus

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Gln Gly Thr Leu Phe Glu Ile Ile Gly Glu Pro Lys Leu Pro Lys Trp
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Phe His Val Glu Cys Leu Glu Asp Pro Lys Arg Leu Tyr Val Glu Pro
35 40 45

Arg Leu Leu Glu Ile Met Phe Gly Lys Asp Gly Glu His Ile Pro His
50 55 60

Leu Glu Ser Met Leu His Thr Leu Ile His Val Asn Val Trp Gly Pro
65 70 75 80

Glu Arg Arg Ala Glu Ile Trp Ile Phe Gly Pro Pro Pro Phe Arg Arg
85 90 95

Asp Val Asp Arg Met Leu Thr Asp Leu Ala His Tyr Cys Arg Met Lys
100 105 110

Leu Met Glu Ile Glu Ala Leu Glu Ala Gly Val Glu Arg Arg Arg Met
115 120 125

Ala Ala His Lys Ala Ala Thr Gln Pro Ala Pro Val Lys Val Arg Glu
130 135 140

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Ala Ala Pro Arg Pro Ala Ser Val Lys Val Pro Glu Thr Ala Thr Gln  
145 150 155 160

Pro Ala Pro Val Lys Val Arg Glu Ala Ala Pro Gln Pro Ala Pro Val  
165 170 175

Gln Glu Val Arg Glu Ala Ala Pro Gln Gln Ala Ser Val Gln Glu Glu  
180 185 190

Val Arg Glu Ala Ala Thr Glu Gln Ala Pro Val Gln Glu Val Arg Glu  
195 200 205

Ala Ala Thr Glu Gln Ala Pro Val Gln Glu Val Ser Glu Ala Ala Thr  
210 215 220

Glu Gln Ala Pro Val Gln Glu Val Asn Glu Ala Ala Thr Glu Gln Ala  
225 230 235 240

Ser Val Gln Ala Val Arg Glu Ala Ala Thr Arg Pro Ala Pro Gly Lys  
245 250 255

Val Arg Lys Ala Ala Thr Gln Pro Ala Pro Val Gln Val Cys Gln Glu  
260 265 270

Ala Thr Gln Leu Ala Pro Val Lys Val Arg Glu Ala Ala Thr Gln Pro  
275 280 285

Ala Ser Gly Lys Val Arg Glu Ala Ala Thr Gln Leu Ala Pro Val Lys  
290 295 300

Val Arg Lys Ala Ala Thr Gln Leu Ala Pro Val Lys Val His Glu Ala  
305 310 315 320

Ala Thr Gln Pro Ala Pro Gly Lys Val Ser Asp Ala Ala Thr Gln Ser  
325 330 335

Ala Ser Val Gln Val Arg Glu Ala Ala Thr Gln Leu Ser Pro Val Glu  
340 345 350

Ala Thr Asp Thr Ser Gln Leu Ala Gln Val Lys Ala Asp Glu Ala Phe  
355 360 365

Ala Gln His Thr Ser Gly Glu Ala His Gln Val Ala Asn Gly Gln Ser  
370 375 380

Pro Ile Glu Val Cys Glu Thr Ala Thr Gly Gln His Ser Leu Asp Val  
385 390 395 400

Ser Arg Ala Leu Ser Gln Lys Cys Pro Glu Val Phe Glu Trp Glu Thr  
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Gln Ser Cys Leu Asp Gly Ser Tyr Val Ile Val Gln Pro Pro Arg Asp  
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Ala Trp Glu Ser Phe Ile Ile Leu  
435 440

<210> 3  
<211> 1063  
<212> DNA

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&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (54)..(704)

&lt;400&gt; 3

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gac gct ccc agg cgg ttt ccg acg ctc gtg caa ctg atg cag cca aaa	104
Asp Ala Pro Arg Arg Phe Pro Thr Leu Val Gln Leu Met Gln Pro Lys	15
	5
gca atg cca gtg gag gtg ctc ggt cac ctc cct aag cgg ttc tcc tgg	152
Ala Met Pro Val Glu Val Leu Gly His Leu Pro Lys Arg Phe Ser Trp	30
	20
ttc cac tct gag ttc ctg aag aat ccg aag gta gtt cgc ctt gag gtt	200
Phe His Ser Glu Phe Leu Lys Asn Pro Lys Val Val Arg Leu Glu Val	45
	35
tgg ctg gtg gaa aag atc ttc ggc cgg ggc gga gaa cgc atc ccg cac	248
Trp Leu Val Glu Lys Ile Phe Gly Arg Gly Gly Glu Arg Ile Pro His	65
	50
gtc cag ggt atg tcc caa atc ttg att cac gtg aat cga ttg gac cct	296
Val Gln Gly Met Ser Gln Ile Leu Ile His Val Asn Arg Leu Asp Pro	80
	70
aac ggc gag gct gag atc ttg gta ttt ggg agg cct tct tac cag gag	344
Asn Gly Glu Ala Glu Ile Leu Val Phe Gly Arg Pro Ser Tyr Gln Glu	95
	85
gac aca atc aag atg atc atg aac ctg gct gac tat cac cgc cag ctc	392
Asp Thr Ile Lys Met Ile Met Asn Leu Ala Asp Tyr His Arg Gln Leu	110
	100
cag gcg aaa ggc tca gga aag gcc ctc gcc cag gat gtc gcc act cag	440
Gln Ala Lys Gly Ser Gly Lys Ala Leu Ala Gln Asp Val Ala Thr Gln	125
	115
aag gcc gag acc cag cgg tct tca ata gaa gtc cgg gag gcc ggg acg	488
Lys Ala Glu Thr Gln Arg Ser Ser Ile Glu Val Arg Glu Ala Gly Thr	145
	130
cag cgt tcg gtg gag gtc cgg gag gcc ggg acc cag cgt tcg gtg gaa	536
Gln Arg Ser Val Glu Val Arg Glu Ala Gly Thr Gln Arg Ser Val Glu	160
	150
gtc cag gag gtc ggg aca cag ggt tct ccg gtg gag gtg cag gag gcc	584
Val Gln Glu Val Gly Thr Gln Gly Ser Pro Val Glu Val Gln Glu Ala	175
	165
ggg acc cag cag tct ctc cag gct gcc aac aag tcg ggg acc cag cga	632
Gly Thr Gln Gln Ser Leu Gln Ala Ala Asn Lys Ser Gly Thr Gln Arg	190
	180
tcc ccc gaa gct gcc agc aag gca gtg acc cag cgg ttt cgc gag gat	680
Ser Pro Glu Ala Ala Ser Lys Ala Val Thr Gln Arg Phe Arg Glu Asp	205
	195
	200

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gcc cgg gac cca gtt act aga tta tgaaggcatc tcaggccctg gagccagagc 734
Ala Arg Asp Pro Val Thr Arg Leu
210 215

cagtcagggg ttaaagtgaa agcccgtatt tccgcccaga agctgggggtt ggggagagga 794
tgtggatttt ttgttttacc ctttctgttg catggttgca aacacaaact tgagttctaa 854
taaagaattg caaagtggaa gcccgcctcc cccctccccc ccgcctccct taagtccagg 914
aagctggggg ggcgaggaag gatgatgtgg attgtttttg ttttaccctt tttgttgaat 974
ggttgccaac ccaaacttga gttttaataa ataattgcct ttccaaaaaa aaaaaaaaaa 1034
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<210> 4
<211> 217
<212> PRT
<213> Homo sapiens

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Lys Ala Met Pro Val Glu Val Leu Gly His Leu Pro Lys Arg Phe Ser
 20 25 30
Trp Phe His Ser Glu Phe Leu Lys Asn Pro Lys Val Val Arg Leu Glu
 35 40 45
Val Trp Leu Val Glu Lys Ile Phe Gly Arg Gly Gly Glu Arg Ile Pro
 50 55 60
His Val Gln Gly Met Ser Gln Ile Leu Ile His Val Asn Arg Leu Asp
 65 70 75 80
Pro Asn Gly Glu Ala Glu Ile Leu Val Phe Gly Arg Pro Ser Tyr Gln
 85 90 95
Glu Asp Thr Ile Lys Met Ile Met Asn Leu Ala Asp Tyr His Arg Gln
 100 105 110
Leu Gln Ala Lys Gly Ser Gly Lys Ala Leu Ala Gln Asp Val Ala Thr
 115 120 125
Gln Lys Ala Glu Thr Gln Arg Ser Ser Ile Glu Val Arg Glu Ala Gly
 130 135 140
Thr Gln Arg Ser Val Glu Val Arg Glu Ala Gly Thr Gln Arg Ser Val
 145 150 155 160
Glu Val Gln Glu Val Gly Thr Gln Gly Ser Pro Val Glu Val Gln Glu
 165 170 175
Ala Gly Thr Gln Gln Ser Leu Gln Ala Ala Asn Lys Ser Gly Thr Gln
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Arg Ser Pro Glu Ala Ala Ser Lys Ala Val Thr Gln Arg Phe Arg Glu
 195 200 205
Asp Ala Arg Asp Pro Val Thr Arg Leu

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<220>  
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 Met Met Val Thr Leu Val Thr Arg Lys Asp Ile Pro Pro Trp Val Lys  
 1 5 10 15  
 gtt cct gaa gac ctg aaa gat cca gaa gta ttc cag gtc cag tcg ctg 154  
 Val Pro Glu Asp Leu Lys Asp Pro Glu Val Phe Gln Val Gln Ser Leu  
 20 25 30  
 gtg ctg aaa tat ctg ttt ggc cca cag gga tct cga atg tct cac atc 202  
 Val Leu Lys Tyr Leu Phe Gly Pro Gln Gly Ser Arg Met Ser His Ile  
 35 40 45  
 gag cag gtg agc cag gcc atg ttt gag ctg aag aac ctg gaa tct ccc 250  
 Glu Gln Val Ser Gln Ala Met Phe Glu Leu Lys Asn Leu Glu Ser Pro  
 50 55 60  
 gaa gaa ctt atc gag gtc ttc att tac ggc tct caa aac aac aag att 298  
 Glu Glu Leu Ile Glu Val Phe Ile Tyr Gly Ser Gln Asn Asn Lys Ile  
 65 70 75 80  
 cgg gct aaa tgg atg ctt cag tcc atg gct gag agg tac cac ctg cgc 346  
 Arg Ala Lys Trp Met Leu Gln Ser Met Ala Glu Arg Tyr His Leu Arg  
 85 90 95  
 cag caa aaa gga gtg ctg aag ctg gag gaa tcc atg aag acc ctg gag 394  
 Gln Gln Lys Gly Val Leu Lys Leu Glu Glu Ser Met Lys Thr Leu Glu  
 100 105 110  
 cta ggc cag tgt atc gag tgaagccagt ttccagtcct tgtgtctccg 442  
 Leu Gly Gln Cys Ile Glu  
 115  
 acctggatgc aggttaagct gtggccagtg tttggttctg gcgggatttt tagctttggtt 502  
 acatcctagc aagatattct ggatccctgc tgcgcattct gatgtgaatc ccaagggttac 562  
 cactctaaat aaaaaataaa attgaagtg 591

<210> 6  
 <211> 118  
 <212> PRT  
 <213> Mus musculus

<400> 6  
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Val Pro Glu Asp Leu Lys Asp Pro Glu Val Phe Gln Val Gln Ser Leu  
20 25 30  
Val Leu Lys Tyr Leu Phe Gly Pro Gln Gly Ser Arg Met Ser His Ile  
35 40 45  
Glu Gln Val Ser Gln Ala Met Phe Glu Leu Lys Asn Leu Glu Ser Pro  
50 55 60  
Glu Glu Leu Ile Glu Val Phe Ile Tyr Gly Ser Gln Asn Asn Lys Ile  
65 70 75 80  
Arg Ala Lys Trp Met Leu Gln Ser Met Ala Glu Arg Tyr His Leu Arg  
85 90 95  
Gln Gln Lys Gly Val Leu Lys Leu Glu Glu Ser Met Lys Thr Leu Glu  
100 105 110  
Leu Gly Gln Cys Ile Glu  
115

<210> 7  
<211> 640  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (15)..(362)

<400> 7  
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1 5 10  
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Trp Val Lys Val Pro Glu Asp Leu Lys Asp Pro Glu Val Phe Gln Val  
15 20 25  
cag acg cgg ctg ctg aaa gcc att ttc ggc ccg gac gga tct cga atc 146  
Gln Thr Arg Leu Leu Lys Ala Ile Phe Gly Pro Asp Gly Ser Arg Ile  
30 35 40  
cct tac atc gag cag gtg agc aag gcc atg ctc gag ctg aag gct ctg 194  
Pro Tyr Ile Glu Gln Val Ser Lys Ala Met Leu Glu Leu Lys Ala Leu  
45 50 55 60  
gag tct tca gac ctc acc gag gtc gtg gtt tac ggc tcc tat ttg tac 242  
Glu Ser Ser Asp Leu Thr Glu Val Val Val Tyr Gly Ser Tyr Leu Tyr  
65 70 75  
aag ctc cgg acc aag tgg atg ctc cag tcc atg gct gag tgg cac cgc 290  
Lys Leu Arg Thr Lys Trp Met Leu Gln Ser Met Ala Glu Trp His Arg  
80 85 90  
cag cgc cag gag cga ggg atg ctc aaa ctt gcc gaa gcc atg aat gcc 338  
Gln Arg Gln Glu Arg Gly Met Leu Lys Leu Ala Glu Ala Met Asn Ala  
95 100 105  
ctc gaa cta ggc cct tgg atg aag tgaaccagtt tccagccaat gcaatgaagc 392



## 701049\_sequence\_listing.txt

Leu Glu Leu Gly Pro Trp Met Lys  
110 115

cgggttgcag agattagggt gtggccagag ctagagtgat tccttaagct tgttttaaaa 452  
tctgctccag cctaaagagt taagggaaaa ccatttggtc ccttaaagag ttaagggaaa 512  
acccttggct ctgagtcttg ttgtgaatat ttctttgatg attgttaata aaaagtgttt 572  
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aaaaaaaaa 640

<210> 8  
<211> 116  
<212> PRT  
<213> Homo sapiens

<400> 8  
Met Gly Thr Leu Pro Ala Arg Arg His Ile Pro Pro Trp Val Lys Val  
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Leu Lys Ala Ile Phe Gly Pro Asp Gly Ser Arg Ile Pro Tyr Ile Glu  
35 40 45  
Gln Val Ser Lys Ala Met Leu Glu Leu Lys Ala Leu Glu Ser Ser Asp  
50 55 60  
Leu Thr Glu Val Val Val Tyr Gly Ser Tyr Leu Tyr Lys Leu Arg Thr  
65 70 75 80  
Lys Trp Met Leu Gln Ser Met Ala Glu Trp His Arg Gln Arg Gln Glu  
85 90 95  
Arg Gly Met Leu Lys Leu Ala Glu Ala Met Asn Ala Leu Glu Leu Gly  
100 105 110  
Pro Trp Met Lys  
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<210> 9  
<211> 1670  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (134)..(1567)

<400> 9  
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tgggagtaca ata atg gag gag tcg gaa ttg gag att ttt aga agt aag 169  
Met Glu Glu Ser Glu Leu Glu Ile Phe Arg Ser Lys  
1 5 10

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ttt	gtt	aga	ggc	tca	tct	gtc	acg	aag	cag	cat	gcc	tgg	cga	aac	cag	217
Phe	Val	Arg	Gly	Ser	Ser	Val	Thr	Lys	Gln	His	Ala	Trp	Arg	Asn	Gln	
		15					20					25				
cac	agc	gag	aag	cgt	tgc	tct	tcc	tcc	atc	agt	tct	ata	tcc	ctg	gac	265
His	Ser	Glu	Lys	Arg	Cys	Ser	Ser	Ser	Ile	Ser	Ser	Ile	Ser	Leu	Asp	
	30					35					40					
aga	atg	cca	tcg	gaa	atc	ttg	gtg	aag	ata	ctt	tct	tac	ttg	gat	gcg	313
Arg	Met	Pro	Ser	Glu	Ile	Leu	Val	Lys	Ile	Leu	Ser	Tyr	Leu	Asp	Ala	
	45				50					55					60	
gtg	acc	ttg	gtg	tgc	att	gga	tgt	gtg	agc	aga	cgc	ttt	tat	cat	ttg	361
Val	Thr	Leu	Val	Cys	Ile	Gly	Cys	Val	Ser	Arg	Arg	Phe	Tyr	His	Leu	
				65					70					75		
gct	gat	gac	aat	ctt	att	tgg	gtc	agg	aag	tac	gca	gct	gca	ttt	aga	409
Ala	Asp	Asp	Asn	Leu	Ile	Trp	Val	Arg	Lys	Tyr	Ala	Ala	Ala	Phe	Arg	
			80					85					90			
tca	aaa	aga	tca	cgt	tgg	aaa	gct	act	tca	gtg	gag	gaa	aca	gcc	aca	457
Ser	Lys	Arg	Ser	Arg	Trp	Lys	Ala	Thr	Ser	Val	Glu	Glu	Thr	Ala	Thr	
		95					100					105				
agt	ctg	agc	ttg	ctg	tca	gtt	tgg	gat	aaa	gaa	gat	gga	tac	tgg	aag	505
Ser	Leu	Ser	Leu	Leu	Ser	Val	Trp	Asp	Lys	Glu	Asp	Gly	Tyr	Trp	Lys	
	110					115					120					
aaa	gaa	tat	att	aca	aag	cag	atc	tca	tct	gtg	aga	gca	gcc	ctc	acc	553
Lys	Glu	Tyr	Ile	Thr	Lys	Gln	Ile	Ser	Ser	Val	Arg	Ala	Ala	Leu	Thr	
	125				130					135					140	
aac	agc	ctc	agt	cct	gtc	aaa	cgc	cgc	aca	agc	ctt	cct	tcg	aaa	acc	601
Asn	Ser	Leu	Ser	Pro	Val	Lys	Arg	Arg	Thr	Ser	Leu	Pro	Ser	Lys	Thr	
				145					150					155		
aaa	gag	tcc	ctc	aga	ata	tct	ggc	tta	ggc	tgg	aca	atc	atc	tta	aga	649
Lys	Glu	Ser	Leu	Arg	Ile	Ser	Gly	Leu	Gly	Trp	Thr	Ile	Ile	Leu	Arg	
			160					165					170			
gaa	gcc	agt	ggc	aaa	gaa	cac	atc	atg	cag	cat	tcg	aat	ctt	tcc	gta	697
Glu	Ala	Ser	Gly	Lys	Glu	His	Ile	Met	Gln	His	Ser	Asn	Leu	Ser	Val	
		175					180					185				
aat	gac	aac	tct	gtc	act	gtt	ttt	tgg	cat	gac	aaa	aat	tgg	cca	cat	745
Asn	Asp	Asn	Ser	Val	Thr	Val	Phe	Trp	His	Asp	Lys	Asn	Trp	Pro	His	
	190					195					200					
gta	gac	acg	ttg	tcc	acc	ctg	gat	ttg	tat	ggc	gcc	aca	cca	att	ttt	793
Val	Asp	Thr	Leu	Ser	Thr	Leu	Asp	Leu	Tyr	Gly	Ala	Thr	Pro	Ile	Phe	
	205				210					215					220	
atg	gag	cag	tat	aaa	ggc	cct	aac	aca	agt	tgt	cca	cga	tgg	ctg	tct	841
Met	Glu	Gln	Tyr	Lys	Gly	Pro	Asn	Thr	Ser	Cys	Pro	Arg	Trp	Leu	Ser	
				225					230					235		
tta	att	gaa	aag	tac	gat	ctg	agt	aat	tta	cgc	aag	tct	gct	atg	att	889
Leu	Ile	Glu	Lys	Tyr	Asp	Leu	Ser	Asn	Leu	Arg	Lys	Ser	Ala	Met	Ile	
			240					245					250			
ggc	tgc	gac	aga	cat	gtt	cgg	gta	ttc	tgt	gta	aat	cct	ggc	ctc	ctg	937
Gly	Cys	Asp	Arg	His	Val	Arg	Val	Phe	Cys	Val	Asn	Pro	Gly	Leu	Leu	

## 701049\_sequence\_listing.txt

255	260	265	
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att cat tcc cat ggc ctt ttc gag aga agc ata atg ggc tca gac act	Ile His Ser His Gly Leu Phe Glu Arg Ser Ile Met Gly Ser Asp Thr	285 290 295 300	1033
att ccc tat aca ttg cct ccc gac act aca ttt gtg gat aac tac cca	Ile Pro Tyr Thr Leu Pro Pro Asp Thr Thr Phe Val Asp Asn Tyr Pro	305 310 315	1081
gac tca atg acc ttt tat gga gat aaa ggc ttt cag ctg cat atc gac	Asp Ser Met Thr Phe Tyr Gly Asp Lys Gly Phe Gln Leu His Ile Asp	320 325 330	1129
att cat ggc agt aag act tac ttc ctg tgt agc acc ttc cac aat ctc	Ile His Gly Ser Lys Thr Tyr Phe Leu Cys Ser Thr Phe His Asn Leu	335 340 345	1177
ttc tgc agg aga gcg ggc att aac aat gga tat gtg aag ttc ttg atg	Phe Cys Arg Arg Ala Gly Ile Asn Asn Gly Tyr Val Lys Phe Leu Met	350 355 360	1225
ata aac tta aaa aat aac aga gaa cac cta cct ctt gtt gga aaa gtt	Ile Asn Leu Lys Asn Asn Arg Glu His Leu Pro Leu Val Gly Lys Val	365 370 375 380	1273
ggc ctt gaa tgg aga act gac tgt tta aat ggc cgt att gag agt tgc	Gly Leu Glu Trp Arg Thr Asp Cys Leu Asn Gly Arg Ile Glu Ser Cys	385 390 395	1321
att gta gtg gat atg acc ttg ctg gat gag gac aag aag ccc atc tgg	Ile Val Val Asp Met Thr Leu Leu Asp Glu Asp Lys Lys Pro Ile Trp	400 405 410	1369
tat gtg agt tct cca gtg tgc ttg aga tct gcc tgc ctt cct gat ttc	Tyr Val Ser Ser Pro Val Cys Leu Arg Ser Ala Cys Leu Pro Asp Phe	415 420 425	1417
ccg cag ccg gct tac tct ttc gag tac atg gac agc gta gga gga gtg	Pro Gln Pro Ala Tyr Ser Phe Glu Tyr Met Asp Ser Val Gly Gly Val	430 435 440	1465
tgc gca gac cta ggg tgg ttt gaa aat acc gat gaa tac ttc att gtc	Cys Ala Asp Leu Gly Trp Phe Glu Asn Thr Asp Glu Tyr Phe Ile Val	445 450 455 460	1513
aga ctg gac att tac ctc agt gta gca aaa tta caa caa tgg ttt ggg	Arg Leu Asp Ile Tyr Leu Ser Val Ala Lys Leu Gln Gln Trp Phe Gly	465 470 475	1561
agg caa taaatgctga gtttagcagta gggagtccttg ttattagtaa gctgtttggt	Arg Gln		1617
ttttacaact ttgttttttat tgaaagttaa aataaagcat atttgtggta ttc			1670

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## 701049\_sequence\_listing.txt

&lt;213&gt; Mus musculus

&lt;400&gt; 10

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Ser 80 Ser 85 Val 90 Thr 95 Lys 100 Gln 105 His 110 Ala 115 Trp 120 Arg 125 Asn 130 Gln 135 His 140 Ser 145 Glu 150 Lys
Arg 155 Cys 160 Ser 165 Ser 170 Ile 175 Ser 180 Ser 185 Ile 190 Ser 195 Leu 200 Asp 205 Arg 210 Met 215 Pro 220 Ser
Glu 225 Ile 230 Leu 235 Val 240 Lys 245 Ile 250 Leu 255 Ser 260 Tyr 265 Leu 270 Asp 275 Ala 280 Val 285 Thr 290 Leu 295
Cys 300 Ile 305 Gly 310 Cys 315 Val 320 Ser 325 Arg 330 Arg 335 Phe 340 Tyr 345 His 350 Leu 355 Ala 360 Asp 365 Asp 370 Asn
Leu 375 Ile 380 Trp 385 Val 390 Arg 395 Lys 400 Tyr 405 Ala 410 Ala 415 Phe 420 Arg 425 Ser 430 Lys 435 Arg 440 Ser
Arg 445 Trp 450 Lys 455 Ala 460 Thr 465 Ser 470 Val 475 Thr 480 Ser 485 Val 490 Glu 495 Thr 500 Leu 505 Ser 510 Leu
Leu 515 Ser 520 Val 525 Asn 530 Thr 535 Lys 540 Gly 545 Tyr 550 Asp 555 Lys 560 Thr 565 Glu 570 Tyr 575 Ile
Thr 580 Lys 585 Gln 590 Ile 595 Ser 600 Ser 605 Val 610 Arg 615 Ala 620 Thr 625 Ser 630 Leu 635 Ser 640 Thr 645
Pro 650 Val 655 Lys 660 Arg 665 Arg 670 Thr 675 Ser 680 Leu 685 Pro 690 Ser 695 Lys 700 Thr 705 Lys 710 Glu 715 Ser 720
Arg 725 Ile 730 Ser 735 Gly 740 Leu 745 Gly 750 Trp 755 Thr 760 Thr 765 Ile 770 Ile 775 Leu 780 Arg 785 Glu 790 Ala 795
Ser 800 Gly 805 Lys 810 Glu 815 Tyr 820 Val 825 Asn 830 Asp 835 Asn 840 Ser 845 Ile 850 Met 855 Gln 860 His 865
Val 870 Thr 875 Val 880 Phe 885 Trp 890 His 895 Asp 900 Lys 905 Asn 910 Trp 915 Pro 920 His 925 Val 930 Asp 935 Thr 940
Leu 945 Thr 950 Asp 955 Val 960 Asn 965 Pro 970 Gly 975 Leu 980 Leu 985 Val 990 Gly 995 Leu 1000 Trp
Gln 1005 Glu 1010 Asn 1015 Gly 1020 Gly 1025 Leu 1030 Ala 1035 Phe 1040 Val 1045 Met 1050 Ala 1055 Asn 1060 Ile 1065
His 1070 Ser 1075 His 1080 Gly 1085 Leu 1090 Phe 1095 Arg 1100 Ser 1105 Ile 1110 Met 1115 Gly 1120 Ser 1125 Asp 1130
Thr 1135 Ile 1140 Pro 1145 Tyr 1150 Thr 1155 Leu 1160 Pro 1165 Asp 1170 Thr 1175 Phe 1180 Val 1185 Asp 1190 Asn 1195
Tyr 1200 Pro 1205 Asp 1210 Ser 1215 Met 1220 Thr 1225 Leu 1230 Pro 1235 Pro 1240 Asp 1245 Thr 1250 Thr 1255

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701049\_sequence\_listing.txt

Phe Tyr Gly Asp Lys Gly Phe Gln Leu His Ile Asp Ile His Gly Ser  
325 330 335  
Lys Thr Tyr Phe Leu Cys Ser Thr Phe His Asn Leu Phe Cys Arg Arg  
340 345 350  
Ala Gly Ile Asn Asn Gly Tyr Val Lys Phe Leu Met Ile Asn Leu Lys  
355 360 365  
Asn Asn Arg Glu His Leu Pro Leu Val Gly Lys Val Gly Leu Glu Trp  
370 375 380  
Arg Thr Asp Cys Leu Asn Gly Arg Ile Glu Ser Cys Ile Val Val Asp  
385 390 395 400  
Met Thr Leu Leu Asp Glu Asp Lys Lys Pro Ile Trp Tyr Val Ser Ser  
405 410 415  
Pro Val Cys Leu Arg Ser Ala Cys Leu Pro Asp Phe Pro Gln Pro Ala  
420 425 430  
Tyr Ser Phe Glu Tyr Met Asp Ser Val Gly Gly Val Cys Ala Asp Leu  
435 440 445  
Gly Trp Phe Glu Asn Thr Asp Glu Tyr Phe Ile Val Arg Leu Asp Ile  
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cac tgg ctc ggc ctc cag acg ctg cgc ggg ccc agc agg ggc ggt ggc 101  
His Trp Leu Gly Leu Gln Thr Leu Arg Gly Pro Ser Arg Gly Gly Gly  
15 20 25  
gcg gcc cgg ggg cgc gcc agg gcc ttt ggg tgc aga aag ggg cca ggg 149  
Ala Ala Arg Gly Arg Ala Arg Ala Phe Gly Cys Arg Lys Gly Pro Gly  
30 35 40  
gtc aag ctt tct gca ggc tct gct gcc ctg agg tgc cat gcc gga ggt 197  
Val Lys Leu Ser Ala Gly Ser Ala Ala Leu Arg Cys His Ala Gly Gly  
45 50 55  
gga cag cac tgg gag agc tct ttc tcc tgc tgt tct ggg ttc ctg gat 245  
Gly Gln His Trp Glu Ser Ser Phe Ser Cys Cys Ser Gly Phe Leu Asp  
60 65 70 75  
gga atg cct tca gaa atc ttg ctg aag ata ttt tcc tac ttg gat gct 293

## 701049\_sequence\_listing.txt

Gly	Met	Pro	Ser	Glu	Ile	Leu	Leu	Lys	Ile	Phe	Ser	Tyr	Leu	Asp	Ala	
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Val	Ser	Leu	Leu	Cys	Thr	Gly	Cys	Val	Ser	Arg	Arg	Phe	Tyr	His	Leu	
			95					100					105			
gcc	aat	gac	aat	ttt	att	tgg	atc	gga	atc	tac	tca	act	gct	ttt	tca	389
Ala	Asn	Asp	Asn	Phe	Ile	Trp	Ile	Gly	Ile	Tyr	Ser	Thr	Ala	Phe	Ser	
		110					115					120				
cct	gca	aga	tca	aat	tgg	aaa	ttt	aat	tca	gta	gag	aag	ata	gct	atg	437
Pro	Ala	Arg	Ser	Asn	Trp	Lys	Phe	Asn	Ser	Val	Glu	Lys	Ile	Ala	Met	
	125					130					135					
tct	atg	agc	ttt	ctg	tca	gtt	cag	gat	aaa	gaa	gct	ggg	tat	tgg	aag	485
Ser	Met	Ser	Phe	Leu	Ser	Val	Gln	Asp	Lys	Glu	Ala	Gly	Tyr	Trp	Lys	
140				145						150					155	
aaa	gaa	tat	atc	aca	aaa	caa	ata	gca	tct	gta	aaa	gcc	gca	cta	gct	533
Lys	Glu	Tyr	Ile	Thr	Lys	Gln	Ile	Ala	Ser	Val	Lys	Ala	Ala	Leu	Ala	
				160					165					170		
gac	att	ctc	aaa	cct	gtc	aac	cct	tac	aca	ggc	ctt	cca	gtt	aag	acc	581
Asp	Ile	Leu	Lys	Pro	Val	Asn	Pro	Tyr	Thr	Gly	Leu	Pro	Val	Lys	Thr	
			175					180					185			
aaa	gag	gcc	ctc	aga	ata	ttt	ggg	tta	ggg	tgg	gca	att	ata	ctg	aaa	629
Lys	Glu	Ala	Leu	Arg	Ile	Phe	Gly	Leu	Gly	Trp	Ala	Ile	Ile	Leu	Lys	
		190					195					200				
gaa	aaa	ggg	gga	aaa	gaa	tat	atc	atg	gag	cat	gtt	gat	ctt	tcc	ata	677
Glu	Lys	Gly	Gly	Lys	Glu	Tyr	Ile	Met	Glu	His	Val	Asp	Leu	Ser	Ile	
	205					210					215					
aat	gac	aca	tca	gtt	act	gtt	ata	tgg	tat	ggc	aaa	aaa	tgg	cca	tgc	725
Asn	Asp	Thr	Ser	Val	Thr	Val	Ile	Trp	Tyr	Gly	Lys	Lys	Trp	Pro	Cys	
220				225						230					235	
cta	gca	tca	ttg	tca	acc	tta	gat	tta	tgt	ggc	atg	aca	cca	gtt	ttt	773
Leu	Ala	Ser	Leu	Ser	Thr	Leu	Asp	Leu	Cys	Gly	Met	Thr	Pro	Val	Phe	
				240					245					250		
acc	gac	tgg	tat	aaa	act	ccc	acc	aaa	cat	aga	ctc	cga	tgg	cat	tct	821
Thr	Asp	Trp	Tyr	Lys	Thr	Pro	Thr	Lys	His	Arg	Leu	Arg	Trp	His	Ser	
			255					260					265			
tta	att	gca	aag	tac	aat	ctg	agt	cat	ttg	acc	ata	tct	acc	atg	att	869
Leu	Ile	Ala	Lys	Tyr	Asn	Leu	Ser	His	Leu	Thr	Ile	Ser	Thr	Met	Ile	
		270					275					280				
ggc	tgt	gac	aga	ctc	att	cgg	atc	ttc	tgc	ctg	cac	cct	ggc	ctc	ctg	917
Gly	Cys	Asp	Arg	Leu	Ile	Arg	Ile	Phe	Cys	Leu	His	Pro	Gly	Leu	Leu	
	285					290					295					
gtg	gga	gtg	tgg	aag	aag	gag	gaa	gaa	ctg	gct	ttt	gtt	atg	gca	aat	965
Val	Gly	Val	Trp	Lys	Lys	Glu	Glu	Glu	Leu	Ala	Phe	Val	Met	Ala	Asn	
300				305						310					315	
ctt	cat	ttt	cat	cac	ctt	gtg	gag	agg	agc	aca	tta	ggc	tcg	gct	act	1013
Leu	His	Phe	His	His	Leu	Val	Glu	Arg	Ser	Thr	Leu	Gly	Ser	Ala	Thr	
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## 701049\_sequence\_listing.txt

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Ile Pro Tyr Glu Leu Pro Pro His Ser Pro Phe Leu Asp Asp Ser Pro
335 340 345

gag tat gga ctg cac ggc tac caa ctc cat gtt gat ctg cac agc ggt 1109
Glu Tyr Gly Leu His Gly Tyr Gln Leu His Val Asp Leu His Ser Gly
350 355 360

ggg gtt ttc tac cta tgt ggt aca ttt cgc aat ctc ttc acc aag aga 1157
Gly Val Phe Tyr Leu Cys Gly Thr Phe Arg Asn Leu Phe Thr Lys Arg
365 370 375

gga aat att gaa aat gga cat gtg aag ctc att gtt ata cat tta aaa 1205
Gly Asn Ile Glu Asn Gly His Val Lys Leu Ile Val Ile His Leu Lys
380 385 390

aat aac aga gaa cac cta cct ctt att gga aaa gtt ggc ctc tcg tgg 1253
Asn Asn Arg Glu His Leu Pro Leu Ile Gly Lys Val Gly Leu Ser Trp
400 405 410

aaa act gat att ttt gat ggc tgt ata aag agt tgt tcc atg atg gac 1301
Lys Thr Asp Ile Phe Asp Gly Cys Ile Lys Ser Cys Ser Met Met Asp
415 420 425

gta act ctt ttg gat gaa cat ggg aaa ccc ttt tgg tgt ttc agt tcc 1349
Val Thr Leu Leu Asp Glu His Gly Lys Pro Phe Trp Cys Phe Ser Ser
430 435 440

ccg gtg tgc ctg aga tcg cct gcc aca ccc tct gac agc tct agc ttc 1397
Pro Val Cys Leu Arg Ser Pro Ala Thr Pro Ser Asp Ser Ser Ser Phe
445 450 455

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Leu Gly Gln Thr Tyr Asn Val Asp Tyr Val Asp Ala Glu Gly Arg Val
460 465 470

cac gtg gag ctg gtg tgg atc aga gag acc gaa gaa tac ctt att gtc 1493
His Val Glu Leu Val Trp Ile Arg Glu Thr Glu Glu Tyr Leu Ile Val
480 485 490

aac ctg gtc ctt tat ctt agt atc gca aaa atc aac cat tgg ttt ggg 1541
Asn Leu Val Leu Tyr Leu Ser Ile Ala Lys Ile Asn His Trp Phe Gly
495 500 505

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Thr Glu Tyr
510

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1665

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<212> PRT
<213> Homo sapiens

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Gln Thr Leu Arg Gly Pro Ser Arg Gly Gly Gly Ala Ala Arg Gly Arg
Page 15

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## 701049\_sequence\_listing.txt

20

25

30

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 Ser Ser Phe Ser Cys Cys Ser Gly Phe Leu Asp Gly Met Pro Ser Glu  
       65                  70                  75                  80  
 Ile Leu Leu Lys Ile Phe Ser Tyr Leu Asp Ala Val Ser Leu Leu Cys  
                   85                  90                  95  
 Thr Gly Cys Val Ser Arg Arg Phe Tyr His Leu Ala Asn Asp Asn Phe  
          100                 105                 110  
 Ile Trp Ile Gly Ile Tyr Ser Thr Ala Phe Ser Pro Ala Arg Ser Asn  
          115                 120                 125  
 Trp Lys Phe Asn Ser Val Glu Lys Ile Ala Met Ser Met Ser Phe Leu  
      130                 135                 140  
 Ser Val Gln Asp Lys Glu Ala Gly Tyr Trp Lys Lys Glu Tyr Ile Thr  
   145                 150                 155                 160  
 Lys Gln Ile Ala Ser Val Lys Ala Ala Leu Ala Asp Ile Leu Lys Pro  
          165                 170                 175  
 Val Asn Pro Tyr Thr Gly Leu Pro Val Lys Thr Lys Glu Ala Leu Arg  
          180                 185                 190  
 Ile Phe Gly Leu Gly Trp Ala Ile Ile Leu Lys Glu Lys Gly Gly Lys  
          195                 200                 205  
 Glu Tyr Ile Met Glu His Val Asp Leu Ser Ile Asn Asp Thr Ser Val  
      210                 215                 220  
 Thr Val Ile Trp Tyr Gly Lys Lys Trp Pro Cys Leu Ala Ser Leu Ser  
   225                 230                 235                 240  
 Thr Leu Asp Leu Cys Gly Met Thr Pro Val Phe Thr Asp Trp Tyr Lys  
          245                 250                 255  
 Thr Pro Thr Lys His Arg Leu Arg Trp His Ser Leu Ile Ala Lys Tyr  
          260                 265                 270  
 Asn Leu Ser His Leu Thr Ile Ser Thr Met Ile Gly Cys Asp Arg Leu  
      275                 280                 285  
 Ile Arg Ile Phe Cys Leu His Pro Gly Leu Leu Val Gly Val Trp Lys  
      290                 295                 300  
 Lys Glu Glu Glu Leu Ala Phe Val Met Ala Asn Leu His Phe His His  
   305                 310                 315                 320  
 Leu Val Glu Arg Ser Thr Leu Gly Ser Ala Thr Ile Pro Tyr Glu Leu  
          325                 330                 335  
 Pro Pro His Ser Pro Phe Leu Asp Asp Ser Pro Glu Tyr Gly Leu His  
          340                 345                 350  
 Gly Tyr Gln Leu His Val Asp Leu His Ser Gly Gly Val Phe Tyr Leu

701049\_sequence\_listing.txt

355

360

365

Cys Gly Thr Phe Arg Asn Leu Phe Thr Lys Arg Gly Asn Ile Glu Asn  
 370 375 380  
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 385 390 395 400  
 Leu Pro Leu Ile Gly Lys Val Gly Leu Ser Trp Lys Thr Asp Ile Phe  
 405 410 415  
 Asp Gly Cys Ile Lys Ser Cys Ser Met Met Asp Val Thr Leu Leu Asp  
 420 425 430  
 Glu His Gly Lys Pro Phe Trp Cys Phe Ser Ser Pro Val Cys Leu Arg  
 435 440 445  
 Ser Pro Ala Thr Pro Ser Asp Ser Ser Ser Phe Leu Gly Gln Thr Tyr  
 450 455 460  
 Asn Val Asp Tyr Val Asp Ala Glu Gly Arg Val His Val Glu Leu Val  
 465 470 475 480  
 Trp Ile Arg Glu Thr Glu Glu Tyr Leu Ile Val Asn Leu Val Leu Tyr  
 485 490 495  
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 tagacactga gtttttttggg tgttgcctaa aaccttttca gaaatccctt ccctcgccat 180  
 cacactgac atg agt gtg ggt ctt cct ggt ccc cac agt ttg cct agt tct 231  
 Met Ser Val Gly Leu Pro Gly Pro His Ser Leu Pro Ser Ser  
 1 5 10  
 gag gaa gca tcg aat tct ggg aac gcc tca tca atg cct gca gtt ttt 279  
 Glu Glu Ala Ser Asn Ser Gly Asn Ala Ser Ser Met Pro Ala Val Phe  
 15 20 25 30  
 cat ccc gag aac tat tct tgc tta caa ggg tct gct act gag atg ctc 327  
 His Pro Glu Asn Tyr Ser Cys Leu Gln Gly Ser Ala Thr Glu Met Leu  
 35 40 45  
 tgc aca gag gct gcc tct cct cgc cct tcc tct gaa gac ctg cct ctt 375  
 Cys Thr Glu Ala Ala Ser Pro Arg Pro Ser Ser Glu Asp Leu Pro Leu  
 50 55 60

## 701049\_sequence\_listing.txt

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Gln	Gly	Ser	Pro	Asp	Ser	Ser	Thr	Ser	Pro	Lys	Gln	Lys	Leu	Ser	Ser	
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cct	gag	gct	gac	aag	ggc	cct	gag	gag	gag	gag	aac	aag	gtc	ctt	gcc	471
Pro	Glu	Ala	Asp	Lys	Gly	Pro	Glu	Glu	Glu	Glu	Asn	Lys	Val	Leu	Ala	
	80					85					90					
agg	aag	cag	aag	atg	cgg	act	gtg	ttc	tct	cag	gcc	cag	ctg	tgt	gca	519
Arg	Lys	Gln	Lys	Met	Arg	Thr	Val	Phe	Ser	Gln	Ala	Gln	Leu	Cys	Ala	
95					100					105					110	
ctc	aag	gac	agg	ttt	cag	aag	cag	aag	tac	ctc	agc	ctc	cag	cag	atg	567
Leu	Lys	Asp	Arg	Phe	Gln	Lys	Gln	Lys	Tyr	Leu	Ser	Leu	Gln	Gln	Met	
				115					120					125		
caa	gaa	ctc	tcc	tcc	att	ctg	aac	ctg	agc	tat	aag	cag	gtt	aag	acc	615
Gln	Glu	Leu	Ser	Ser	Ile	Leu	Asn	Leu	Ser	Tyr	Lys	Gln	Val	Lys	Thr	
			130					135					140			
tgg	ttt	caa	aac	caa	agg	gtg	aag	tgc	aag	cgg	tgg	cag	aaa	aac	cag	663
Trp	Phe	Gln	Asn	Gln	Arg	Val	Lys	Cys	Lys	Arg	Trp	Gln	Lys	Asn	Gln	
		145					150					155				
tgg	ttg	aag	act	agc	aat	ggt	ctg	att	cag	aag	ggc	tca	gca	cca	gtg	711
Trp	Leu	Lys	Thr	Ser	Asn	Gly	Leu	Ile	Gln	Lys	Gly	Ser	Ala	Pro	Val	
	160					165					170					
gag	tat	ccc	agc	atc	cat	tgc	agc	tat	ccc	cag	ggc	tat	ctg	gtg	aac	759
Glu	Tyr	Pro	Ser	Ile	His	Cys	Ser	Tyr	Pro	Gln	Gly	Tyr	Leu	Val	Asn	
175					180					185					190	
gca	tct	gga	agc	ctt	tcc	atg	tgg	ggc	agc	cag	act	tgg	acc	aac	cca	807
Ala	Ser	Gly	Ser	Leu	Ser	Met	Trp	Gly	Ser	Gln	Thr	Trp	Thr	Asn	Pro	
				195				200						205		
act	tgg	agc	agc	cag	acc	tgg	acc	aac	cca	act	tgg	aac	aac	cag	acc	855
Thr	Trp	Ser	Ser	Gln	Thr	Trp	Thr	Asn	Pro	Thr	Trp	Asn	Asn	Gln	Thr	
			210					215					220			
tgg	acc	aac	cca	act	tgg	agc	agc	cag	gcc	tgg	acc	gct	cag	tcc	tgg	903
Trp	Thr	Asn	Pro	Thr	Trp	Ser	Ser	Gln	Ala	Trp	Thr	Ala	Gln	Ser	Trp	
		225					230					235				
aac	ggc	cag	cct	tgg	aat	gct	gct	ccg	ctc	cat	aac	ttc	ggg	gag	gac	951
Asn	Gly	Gln	Pro	Trp	Asn	Ala	Ala	Pro	Leu	His	Asn	Phe	Gly	Glu	Asp	
	240					245					250					
ttt	ctg	cag	cct	tac	gta	cag	ttg	cag	caa	aac	ttc	tct	gcc	agt	gat	999
Phe	Leu	Gln	Pro	Tyr	Val	Gln	Leu	Gln	Gln	Asn	Phe	Ser	Ala	Ser	Asp	
255					260					265					270	
ttg	gag	gtg	aat	ttg	gaa	gcc	act	agg	gaa	agc	cat	gcg	cat	ttt	agc	1047
Leu	Glu	Val	Asn	Leu	Glu	Ala	Thr	Arg	Glu	Ser	His	Ala	His	Phe	Ser	
				275				280						285		
acc	cca	caa	gcc	ttg	gaa	tta	ttc	ctg	aac	tac	tct	gtg	act	cca	cca	1095
Thr	Pro	Gln	Ala	Leu	Glu	Leu	Phe	Leu	Asn	Tyr	Ser	Val	Thr	Pro	Pro	
			290					295					300			
ggt	gaa	ata	tgagacttac gcaacatctg ggcttaaagt cagggcaaag													1144
Gly	Glu	Ile														
		305														

701049\_sequence\_listing.txt

```

ccagggttcct tccttcttcc aaatattttc atattttttt taaagattta tttattcatt 1204
atatgtaagt acactgtagc tgtcttcaga cactccagaa gagggcgtca gatcttggtta 1264
cgtatgggttg tgagccacca tgtgggtgct gggatttgaa ctcttgacct tcggaagagc 1324
agtcgggtgc tcttatccac tgagccatct caccagcccc tggtttattt ttttaattat 1384
tatttgcttt ttgtttatca agacagggtt tctctgcata gctctaattg tctttgaact 1444
agctctgcag accagcctgg ccttgaactc agagatctgc ccacttatct ttgcctcctg 1504
aatgctggga ccaaagggtg cataccacca cacctggcat atatattggt tatttctatt 1564
tctattttta ttggtgccag agcaaacctt ggacttagaa catgctgggc accaactcaa 1624
cttctgagct ctatttacia cttgggtgtg tagtgtattt gtcttagttc tgaatttgct 1684
cttttttttag tgttaactct aggctttgga gacagtgagg tgcataact ctctccttcc 1744
caagaataag tgcttgaaca cccttaccac cgcccaccca cccatgctag tcttttttct 1804
tagaagcgtg ggtcttggtt tacactgtgt cattttgagg ggtgagggtt aaaagtatat 1864
acaaagtata acgatatggt ggctactctc gaggatgaga cagaaggacc aggagtttga 1924
gggtagctca gatatgcaat aagttcaagg ccaacctgta ctatgtttta atagtaagac 1984
agcatctcga taaaataata aaactaaagt ctcaacaaaa taaaagcttt cacctattaa 2044
ggtgcttgct tgtccttgga gtcccccaag agtaactgct atgttaatat ctgtagaaag 2104
atgtttatat ttgactgtac catgatgaac cgatgccagc tggactagtt taaacaaaat 2164
aaaacactaa ttttaccttt 2184

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<210> 14  
 <211> 305  
 <212> PRT  
 <213> Mus musculus

<400> 14  
 Met Ser Val Gly Leu Pro Gly Pro His Ser Leu Pro Ser Ser Glu Glu  
 1 5 10 15  
 Ala Ser Asn Ser Gly Asn Ala Ser Ser Met Pro Ala Val Phe His Pro  
 20 25 30  
 Glu Asn Tyr Ser Cys Leu Gln Gly Ser Ala Thr Glu Met Leu Cys Thr  
 35 40 45  
 Glu Ala Ala Ser Pro Arg Pro Ser Ser Glu Asp Leu Pro Leu Gln Gly  
 50 55 60  
 Ser Pro Asp Ser Ser Thr Ser Pro Lys Gln Lys Leu Ser Ser Pro Glu  
 65 70 75 80  
 Ala Asp Lys Gly Pro Glu Glu Glu Glu Asn Lys Val Leu Ala Arg Lys  
 85 90 95  
 Gln Lys Met Arg Thr Val Phe Ser Gln Ala Gln Leu Cys Ala Leu Lys

## 701049\_sequence\_listing.txt

100

105

110

Asp Arg Phe Gln Lys Gln Lys Tyr Leu Ser Leu Gln Gln Met Gln Glu  
 115 120 125  
 Leu Ser Ser Ile Leu Asn Leu Ser Tyr Lys Gln Val Lys Thr Trp Phe  
 130 135 140  
 Gln Asn Gln Arg Val Lys Cys Lys Arg Trp Gln Lys Asn Gln Trp Leu  
 145 150 155 160  
 Lys Thr Ser Asn Gly Leu Ile Gln Lys Gly Ser Ala Pro Val Glu Tyr  
 165 170 175  
 Pro Ser Ile His Cys Ser Tyr Pro Gln Gly Tyr Leu Val Asn Ala Ser  
 180 185 190  
 Gly Ser Leu Ser Met Trp Gly Ser Gln Thr Trp Thr Asn Pro Thr Trp  
 195 200 205  
 Ser Ser Gln Thr Trp Thr Asn Pro Thr Trp Asn Asn Gln Thr Trp Thr  
 210 215 220  
 Asn Pro Thr Trp Ser Ser Gln Ala Trp Thr Ala Gln Ser Trp Asn Gly  
 225 230 235 240  
 Gln Pro Trp Asn Ala Ala Pro Leu His Asn Phe Gly Glu Asp Phe Leu  
 245 250 255  
 Gln Pro Tyr Val Gln Leu Gln Gln Asn Phe Ser Ala Ser Asp Leu Glu  
 260 265 270  
 Val Asn Leu Glu Ala Thr Arg Glu Ser His Ala His Phe Ser Thr Pro  
 275 280 285  
 Gln Ala Leu Glu Leu Phe Leu Asn Tyr Ser Val Thr Pro Pro Gly Glu  
 290 295 300  
 Ile  
 305

<210> 15  
 <211> 2114  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (217)..(1131)

<400> 15  
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 gttattatgc aggcaactca ctttatccca atttcttgat acttttcctt ctggagggtcc 120  
 tattttctcta acatcttcca gaaaagtctt aaagctgcct taaccttttt tccagtccac 180  
 ctcttaaatt ttttcctcct cttcctctat actaac atg agt gtg gat cca gct 234  
 Met Ser Val Asp Pro Ala  
 1 5

## 701049\_sequence\_listing.txt

tgt	ccc	caa	agc	ttg	cct	tgc	ttt	gaa	gca	tcc	gac	tgt	aaa	gaa	tct	282
Cys	Pro	Gln	Ser	Leu	Pro	Cys	Phe	Glu	Ala	Ser	Asp	Cys	Lys	Glu	Ser	
		10						15					20			
tca	cct	atg	cct	gtg	att	tgt	ggg	cct	gaa	gaa	aac	tat	cca	tcc	ttg	330
Ser	Pro	Met	Pro	Val	Ile	Cys	Gly	Pro	Glu	Glu	Asn	Tyr	Pro	Ser	Leu	
		25					30					35				
caa	atg	tct	tct	gct	gag	atg	cct	cac	acg	gag	act	gtc	tct	cct	ctt	378
Gln	Met	Ser	Ser	Ala	Glu	Met	Pro	His	Thr	Glu	Thr	Val	Ser	Pro	Leu	
	40					45					50					
ccc	tcc	tcc	atg	gat	ctg	ctt	att	cag	gac	agc	cct	gat	tct	tcc	acc	426
Pro	Ser	Ser	Met	Asp	Leu	Leu	Ile	Gln	Asp	Ser	Pro	Asp	Ser	Ser	Thr	
55					60					65					70	
agt	ccc	aaa	ggc	aaa	caa	ccc	act	tct	gca	gag	aat	agt	gtc	gca	aaa	474
Ser	Pro	Lys	Gly	Lys	Gln	Pro	Thr	Ser	Ala	Glu	Asn	Ser	Val	Ala	Lys	
				75					80					85		
aag	gaa	gac	aag	gtc	cca	gtc	aag	aaa	cag	aag	acc	aga	act	gtg	ttc	522
Lys	Glu	Asp	Lys	Val	Pro	Val	Lys	Lys	Gln	Lys	Thr	Arg	Thr	Val	Phe	
			90					95					100			
tct	tcc	acc	cag	ctg	tgt	gta	ctc	aat	gat	aga	ttt	cag	aga	cag	aaa	570
Ser	Ser	Thr	Gln	Leu	Cys	Val	Leu	Asn	Asp	Arg	Phe	Gln	Arg	Gln	Lys	
		105					110					115				
tac	ctc	agc	ctc	cag	cag	atg	caa	gaa	ctc	tcc	aac	atc	ctg	aac	ctc	618
Tyr	Leu	Ser	Leu	Gln	Gln	Met	Gln	Glu	Leu	Ser	Asn	Ile	Leu	Asn	Leu	
	120					125					130					
agc	tac	aaa	cag	gtg	aag	acc	tgg	ttc	cag	aac	cag	aga	atg	aaa	tct	666
Ser	Tyr	Lys	Gln	Val	Lys	Thr	Trp	Phe	Gln	Asn	Gln	Arg	Met	Lys	Ser	
135					140				145					150		
aag	agg	tgg	cag	aaa	aac	aac	tgg	ccg	aag	aat	agc	aat	ggg	gtg	acg	714
Lys	Arg	Trp	Gln	Lys	Asn	Asn	Trp	Pro	Lys	Asn	Ser	Asn	Gly	Val	Thr	
				155					160					165		
cag	aag	gcc	tca	gca	cct	acc	tac	ccc	agc	ctc	tac	tct	tcc	tac	cac	762
Gln	Lys	Ala	Ser	Ala	Pro	Thr	Tyr	Pro	Ser	Leu	Tyr	Ser	Ser	Tyr	His	
			170					175					180			
cag	gga	tgc	ctg	gtg	aac	ccg	act	ggg	aac	ctt	cca	atg	tgg	agc	aac	810
Gln	Gly	Cys	Leu	Val	Asn	Pro	Thr	Gly	Asn	Leu	Pro	Met	Trp	Ser	Asn	
		185					190					195				
cag	acc	tgg	aac	aat	tca	acc	tgg	agc	aac	cag	acc	cag	aac	atc	cag	858
Gln	Thr	Trp	Asn	Asn	Ser	Thr	Trp	Ser	Asn	Gln	Thr	Gln	Asn	Ile	Gln	
	200					205					210					
tcc	tgg	agc	aac	cac	tcc	tgg	aac	act	cag	acc	tgg	tgc	acc	caa	tcc	906
Ser	Trp	Ser	Asn	His	Ser	Trp	Asn	Thr	Gln	Thr	Trp	Cys	Thr	Gln	Ser	
215					220					225					230	
tgg	aac	aat	cag	gcc	tgg	aac	agt	ccc	ttc	tat	aac	tgt	gga	gag	gaa	954
Trp	Asn	Asn	Gln	Ala	Trp	Asn	Ser	Pro	Phe	Tyr	Asn	Cys	Gly	Glu	Glu	
				235					240					245		
tct	ctg	cag	tcc	tgc	atg	cag	ttc	cag	cca	aat	tct	cct	gcc	agt	gac	1002
Ser	Leu	Gln	Ser	Cys	Met	Gln	Phe	Gln	Pro	Asn	Ser	Pro	Ala	Ser	Asp	
			250					255					260			

701049\_sequence\_listing.txt

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ttg gag gct gct ttg gaa gct gct ggg gaa ggc ctt aat gta ata cag 1050
Leu Glu Ala Ala Leu Glu Ala Ala Gly Glu Gly Leu Asn Val Ile Gln
265 270 275

cag acc act agg tat ttt agt act cca caa acc atg gat tta ttc cta 1098
Gln Thr Thr Arg Tyr Phe Ser Thr Pro Gln Thr Met Asp Leu Phe Leu
280 285 290

aac tac tcc atg aac atg caa cct gaa gac gtg tgaagatgag tgaaactgat 1151
Asn Tyr Ser Met Asn Met Gln Pro Glu Asp Val
295 300 305

attactcaat ttcagtctgg acactggctg aatccttcct ctcccctcct cccatccctc 1211
ataggatttt tcttgtttgg aaaccacgtg ttctggtttc catgatgcct atccagtcaa 1271
tctcatggag ggtggagtat ggttggagcc taatcagcga ggtttctttt tttttttttc 1331
ctattggatc ttcctggaga aaatactttt tttttttttt ttgagacgga gtcttgctct 1391
gtcgcccagg ctggagtgca gtggcgcggt cttggctcac tgcaagctcc gcctcccggg 1451
ttcacgccat tctcctgcct cagcctcccg agcagctggg actacaggcg cccgccacct 1511
cgccccggcta atattttgta tttttagtag agacagggtt tcactgtgtt agccaggatg 1571
gtctcgatct cctgaccttg tgatccgccc gcctcggcct ccctaacagc tgggattaca 1631
ggcgtgagcc accgcgccct gcctagaaaa gacattttta taaccttggc tgctaaggac 1691
aacattgata gaagccgtct ctggctatag ataagtagat ctaatactag tttggatatc 1751
tttaggggtt agaatctaac ctcaagaata agaaatacaa gtacgaattg gtgatgaaga 1811
tgtattcgta ttgtttggga ttgggaggct ttgcttattt ttttaaaact attgaggtaa 1871
agggttaagc tgtaacatac ttaattgatt tcttaccgtt tttggctctg ttttgctata 1931
tcccctaatt tgttggttgt gctaattctt gtagaaagag gtcttgtatt tgctgcatcg 1991
taatgacatg agtactactt tagttgggtt aagttcaaata gaatgaaaca aatatttttc 2051
ctttagttga ttttaccctg atttcaccga gtgtttcgat gagtaaataat acagcttaaa 2111
cat 2114

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<210> 16  
 <211> 305  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Ser Val Asp Pro Ala Cys Pro Gln Ser Leu Pro Cys Phe Glu Ala  
 1 5 10 15  
 Ser Asp Cys Lys Glu Ser Ser Pro Met Pro Val Ile Cys Gly Pro Glu  
 20 25 30  
 Glu Asn Tyr Pro Ser Leu Gln Met Ser Ser Ala Glu Met Pro His Thr  
 35 40 45



## 701049\_sequence\_listing.txt

Glu Thr Val Ser Pro Leu Pro Ser Ser Met Asp Leu Leu Ile Gln Asp  
 50 55 60  
 Ser Pro Asp Ser Ser Thr Ser Pro Lys Gly Lys Gln Pro Thr Ser Ala  
 65 70 75 80  
 Glu Asn Ser Val Ala Lys Lys Glu Asp Lys Val Pro Val Lys Lys Gln  
 85 90 95  
 Lys Thr Arg Thr Val Phe Ser Ser Thr Gln Leu Cys Val Leu Asn Asp  
 100 105 110  
 Arg Phe Gln Arg Gln Lys Tyr Leu Ser Leu Gln Gln Met Gln Glu Leu  
 115 120 125  
 Ser Asn Ile Leu Asn Leu Ser Tyr Lys Gln Val Lys Thr Trp Phe Gln  
 130 135 140  
 Asn Gln Arg Met Lys Ser Lys Arg Trp Gln Lys Asn Asn Trp Pro Lys  
 145 150 155 160  
 Asn Ser Asn Gly Val Thr Gln Lys Ala Ser Ala Pro Thr Tyr Pro Ser  
 165 170 175  
 Leu Tyr Ser Ser Tyr His Gln Gly Cys Leu Val Asn Pro Thr Gly Asn  
 180 185 190  
 Leu Pro Met Trp Ser Asn Gln Thr Trp Asn Asn Ser Thr Trp Ser Asn  
 195 200 205  
 Gln Thr Gln Asn Ile Gln Ser Trp Ser Asn His Ser Trp Asn Thr Gln  
 210 215 220  
 Thr Trp Cys Thr Gln Ser Trp Asn Asn Gln Ala Trp Asn Ser Pro Phe  
 225 230 235 240  
 Tyr Asn Cys Gly Glu Glu Ser Leu Gln Ser Cys Met Gln Phe Gln Pro  
 245 250 255  
 Asn Ser Pro Ala Ser Asp Leu Glu Ala Ala Leu Glu Ala Ala Gly Glu  
 260 265 270  
 Gly Leu Asn Val Ile Gln Gln Thr Thr Arg Tyr Phe Ser Thr Pro Gln  
 275 280 285  
 Thr Met Asp Leu Phe Leu Asn Tyr Ser Met Asn Met Gln Pro Glu Asp  
 290 295 300  
 Val  
 305

<210> 17  
 <211> 1078  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (178)..(858)

<400> 17

## 701049\_sequence\_listing.txt

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caggggtcgg gcaggtggga gggggaagct cacatctccg ccctctgctg cctctggggg 60
tagggagcat cctaaccccc aactgtccgg tcagatccgc ctactgcccc tcatcagact 120
gctactcctg ggagcacagc acctgctctt tacacctctt ccttgagctg ctgggga 177
atg gct ttg cct aca aag tct agc atc ttg gac ctg agc tcc ggc acc 225
Met Ala Leu Pro Thr Lys Ser Ser Ile Leu Asp Leu Ser Ser Gly Thr
1 5 10 15
cca tgc acc aga tct cca gag gaa agt cac gag gct tgg gca cag tgc 273
Pro Cys Thr Arg Ser Pro Glu Glu Ser His Glu Ala Trp Ala Gln Cys
20 25 30
aaa gat gct ggc agg cag cta ccc gag tac aag gca gtg gtg gtg ggt 321
Lys Asp Ala Gly Arg Gln Leu Pro Glu Tyr Lys Ala Val Val Val Gly
35 40 45
gca agt ggt gtt ggt aaa agt gct ctc acc atc cag atg act cac caa 369
Ala Ser Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Met Thr His Gln
50 55 60
tgc ttc gtg aaa gac cat gac ccc act atc caa gat tcc tac tgg aag 417
Cys Phe Val Lys Asp His Asp Pro Thr Ile Gln Asp Ser Tyr Trp Lys
65 70 75 80
gaa gtg gcc agg gac aac gga ggc tac att cta aat gtt ctg gat aca 465
Glu Val Ala Arg Asp Asn Gly Gly Tyr Ile Leu Asn Val Leu Asp Thr
85 90 95
tct ggg cag gat att cac cgg gct ctg cgt gac cag tgc ttg gca tct 513
Ser Gly Gln Asp Ile His Arg Ala Leu Arg Asp Gln Cys Leu Ala Ser
100 105 110
ggt gat ggt gtg ctg ggc gtc ttt gct ctt gac gac ccc tcg tct ctg 561
Gly Asp Gly Val Leu Gly Val Phe Ala Leu Asp Asp Pro Ser Ser Leu
115 120 125
gac cag ttg cag cag ata tgg tcc acc tgg acc cct cac cac aag cag 609
Asp Gln Leu Gln Gln Ile Trp Ser Thr Trp Thr Pro His His Lys Gln
130 135 140
cct ctg gta cta gtg ggc aac aag tgt gac ctg gtg acc act gct gga 657
Pro Leu Val Leu Val Gly Asn Lys Cys Asp Leu Val Thr Thr Ala Gly
145 150 155 160
gat gct cat gct gcc gca gcc ctc ctt gct cac aag ttg ggg gcc ccc 705
Asp Ala His Ala Ala Ala Leu Leu Ala His Lys Leu Gly Ala Pro
165 170 175
ttg gtg aag acc tca gcc aag acg cgg caa ggt gtg gag gaa gcc ttt 753
Leu Val Lys Thr Ser Ala Lys Thr Arg Gln Gly Val Glu Glu Ala Phe
180 185 190
gcc ctg ctt gtc cat gag att cag agg gcc cag gag gct gtg gcc gaa 801
Ala Leu Leu Val His Glu Ile Gln Arg Ala Gln Glu Ala Val Ala Glu
195 200 205
tca agc aag aag acc cga cac cag aaa gcc gtg tgt agc tgt ggc tgc 849
Ser Ser Lys Lys Thr Arg His Gln Lys Ala Val Cys Ser Cys Gly Cys
210 215 220
tct gta gcc tgaagatctt tgtctagcaa attgaccctt gtctcatgtc 898

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701049\_sequence\_listing.txt

Ser Val Ala  
225

aaggtgacaa ttctcttgta ataagatctc cctctccgac caagttacca cagacatctt 958  
tttattgtca ttgtgtgaga agttacgtgg taacatggga catccctcat tgactgtgtt 1018  
ttatgaaact ctatgcaaaa tttaaataaat gttttcagga ttcaaagctt cctttataacc 1078

<210> 18  
<211> 227  
<212> PRT  
<213> Mus musculus

<400> 18  
Met Ala Leu Pro Thr Lys Ser Ser Ile Leu Asp Leu Ser Ser Gly Thr  
1 5 10 15  
Pro Cys Thr Arg Ser Pro Glu Glu Ser His Glu Ala Trp Ala Gln Cys  
20 25 30  
Lys Asp Ala Gly Arg Gln Leu Pro Glu Tyr Lys Ala Val Val Val Gly  
35 40 45  
Ala Ser Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Met Thr His Gln  
50 55 60  
Cys Phe Val Lys Asp His Asp Pro Thr Ile Gln Asp Ser Tyr Trp Lys  
65 70 75 80  
Glu Val Ala Arg Asp Asn Gly Gly Tyr Ile Leu Asn Val Leu Asp Thr  
85 90 95  
Ser Gly Gln Asp Ile His Arg Ala Leu Arg Asp Gln Cys Leu Ala Ser  
100 105 110  
Gly Asp Gly Val Leu Gly Val Phe Ala Leu Asp Asp Pro Ser Ser Leu  
115 120 125  
Asp Gln Leu Gln Gln Ile Trp Ser Thr Trp Thr Pro His His Lys Gln  
130 135 140  
Pro Leu Val Leu Val Gly Asn Lys Cys Asp Leu Val Thr Thr Ala Gly  
145 150 155 160  
Asp Ala His Ala Ala Ala Ala Leu Leu Ala His Lys Leu Gly Ala Pro  
165 170 175  
Leu Val Lys Thr Ser Ala Lys Thr Arg Gln Gly Val Glu Glu Ala Phe  
180 185 190  
Ala Leu Leu Val His Glu Ile Gln Arg Ala Gln Glu Ala Val Ala Glu  
195 200 205  
Ser Ser Lys Lys Thr Arg His Gln Lys Ala Val Cys Ser Cys Gly Cys  
210 215 220

Ser Val Ala  
225

## 701049\_sequence\_listing.txt

<210> 19  
 <211> 1266  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (252)..(950)

<400> 19  
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 tatatatagc atgcaaattg gaagggtgac agcacacaat aggcattcaa taaatgttga 120  
 aataatgaca cccactgtc tccttgccct caaatgggtct cccctaacgt atcccctgtt 180  
 gtcttgcttc ttctcttccc acttgcagag cctgctgccc acgtctcttc cctgagctgc 240  
 ctgctgggggt c atg gag ctg cca aca aag cct ggc acc ttc gac ctg ggc 290  
                   Met Glu Leu Pro Thr Lys Pro Gly Thr Phe Asp Leu Gly  
                   1                  5                  10  
 ctg gcc aca tgg agc cct tcc ttc cag ggg gaa acc cac cgg gct cag 338  
 Leu Ala Thr Trp Ser Pro Ser Phe Gln Gly Glu Thr His Arg Ala Gln  
                   15                  20                  25  
 gca cgc cgc agg gat gtt ggc agg cag ctg cct gag tac aag gct gtg 386  
 Ala Arg Arg Arg Asp Val Gly Arg Gln Leu Pro Glu Tyr Lys Ala Val  
                   30                  35                  40                  45  
 gtg gtg ggc gcc agt ggc gtg ggc aag agt gcg ctg acc atc cag ctg 434  
 Val Val Gly Ala Ser Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Leu  
                   50                  55                  60  
 aac cac cag tgc ttc gtg gag gac cac gac ccc acc atc cag gat tcc 482  
 Asn His Gln Cys Phe Val Glu Asp His Asp Pro Thr Ile Gln Asp Ser  
                   65                  70                  75  
 tac tgg aag gag ttg acc ctg gac agt ggg gac tgc att ctg aat gtg 530  
 Tyr Trp Lys Glu Leu Thr Leu Asp Ser Gly Asp Cys Ile Leu Asn Val  
                   80                  85                  90  
 ctg gac aca gca ggg cag gcc atc cat agg gcc ctg cgt gac cag tgc 578  
 Leu Asp Thr Ala Gly Gln Ala Ile His Arg Ala Leu Arg Asp Gln Cys  
                   95                  100                  105  
 ctg gct gtc tgt gat ggt gtg ctg ggc gtc ttc gct ctc gat gac ccc 626  
 Leu Ala Val Cys Asp Gly Val Leu Gly Val Phe Ala Leu Asp Asp Pro  
                   110                  115                  120                  125  
 tcg tct ctg atc cag ctg cag cag ata tgg gcc acc tgg ggc cct cac 674  
 Ser Ser Leu Ile Gln Leu Gln Gln Ile Trp Ala Thr Trp Gly Pro His  
                   130                  135                  140  
 ccc gcc cag ccc ctt gtc ctc gtg ggc aac aag tgt gac ctt gtg acc 722  
 Pro Ala Gln Pro Leu Val Leu Val Gly Asn Lys Cys Asp Leu Val Thr  
                   145                  150                  155  
 act gct gga gat gct cat gcc gct gct gca gcc ctc gca cac agc tgg 770  
 Thr Ala Gly Asp Ala His Ala Ala Ala Ala Leu Ala His Ser Trp  
                   160                  165                  170  
 ggg gcc cac ttc gtg gag acc tcg gcc aaa aca cgg caa ggc gtg gag 818

## 701049\_sequence\_listing.txt

Gly Ala His Phe Val Glu Thr Ser Ala Lys Thr Arg Gln Gly Val Glu  
 175 180 185

gag gcc ttt tcc ctg ctg gtc cat gag atc cag agg gtc cag gag gcc 866  
 Glu Ala Phe Ser Leu Leu Val His Glu Ile Gln Arg Val Gln Glu Ala  
 190 195 200 205

atg gcg aag gag ccc atg gca agg tcc tgt agg gag aag acc cgg cac 914  
 Met Ala Lys Glu Pro Met Ala Arg Ser Cys Arg Glu Lys Thr Arg His  
 210 215 220

cag aag gcc acc tgc cac tgt ggc tgc tct gtg gcc tgaaggctctt 960  
 Gln Lys Ala Thr Cys His Cys Gly Cys Ser Val Ala  
 225 230

ggccaagaaa tgtagacctt tccccaggcc aggggtgattg ttcatttgac atgagacccc 1020

tgaggcaact agctttgagg gacacatcag gtatactagg gaaagatgga catctctctt 1080

gttttcactt ggtgaggggc tttttggttaa catgggagtg cctaattgttg cttttgttat 1140

gtcaagttga aagattttgt gcaaaattaa ataaatgggtg ttttgggttt caaagctgcc 1200

tccatgccga gtgttggtgtg ggtgggagtg agactgggta gaatgttact tgagttgtga 1260

gaattc 1266

<210> 20  
 <211> 233  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Met Glu Leu Pro Thr Lys Pro Gly Thr Phe Asp Leu Gly Leu Ala Thr  
 1 5 10 15

Trp Ser Pro Ser Phe Gln Gly Glu Thr His Arg Ala Gln Ala Arg Arg  
 20 25 30

Arg Asp Val Gly Arg Gln Leu Pro Glu Tyr Lys Ala Val Val Val Gly  
 35 40 45

Ala Ser Gly Val Gly Lys Ser Ala Leu Thr Ile Gln Leu Asn His Gln  
 50 55 60

Cys Phe Val Glu Asp His Asp Pro Thr Ile Gln Asp Ser Tyr Trp Lys  
 65 70 75 80

Glu Leu Thr Leu Asp Ser Gly Asp Cys Ile Leu Asn Val Leu Asp Thr  
 85 90 95

Ala Gly Gln Ala Ile His Arg Ala Leu Arg Asp Gln Cys Leu Ala Val  
 100 105 110

Cys Asp Gly Val Leu Gly Val Phe Ala Leu Asp Asp Pro Ser Ser Leu  
 115 120 125

Ile Gln Leu Gln Gln Ile Trp Ala Thr Trp Gly Pro His Pro Ala Gln  
 130 135 140

Pro Leu Val Leu Val Gly Asn Lys Cys Asp Leu Val Thr Thr Ala Gly  
 145 150 155 160

701049\_sequence\_listing.txt

Asp Ala His Ala Ala Ala Ala Leu Ala His Ser Trp Gly Ala His  
165 170 175  
Phe Val Glu Thr Ser Ala Lys Thr Arg Gln Gly Val Glu Glu Ala Phe  
180 185 190  
Ser Leu Leu Val His Glu Ile Gln Arg Val Gln Glu Ala Met Ala Lys  
195 200 205  
Glu Pro Met Ala Arg Ser Cys Arg Glu Lys Thr Arg His Gln Lys Ala  
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Thr Cys His Cys Gly Cys Ser Val Ala  
225 230

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<211> 1063  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (177)..(872)

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gagttgctgg cctggctgcc tacctgcttt cctgagatcc agggactttt cccaga atg 179  
Met  
1  
gct ttg ggt gac ctc ctg ctg tct gtc ctc tct gcc cag gaa atg aat 227  
Ala Leu Gly Asp Leu Leu Leu Ser Val Leu Ser Ala Gln Glu Met Asn  
5 10 15  
gcc ctt cgt ggc cag gtg ggc ggg gac gtc aat gtg gag atg gac gcc 275  
Ala Leu Arg Gly Gln Val Gly Gly Asp Val Asn Val Glu Met Asp Ala  
20 25 30  
gcc ccc ggt gtg gac ctg agc cgc atc ctg aac gag atg cgg gat cag 323  
Ala Pro Gly Val Asp Leu Ser Arg Ile Leu Asn Glu Met Arg Asp Gln  
35 40 45  
tat gag aag atg gcg gag aag aac cgc aag gat gct gag gaa tgg ttc 371  
Tyr Glu Lys Met Ala Glu Lys Asn Arg Lys Asp Ala Glu Glu Trp Phe  
50 55 60 65  
ttc acc aag aca gag gag ctg aac cga gaa gtg gcc acc aac acg gag 419  
Phe Thr Lys Thr Glu Glu Leu Asn Arg Glu Val Ala Thr Asn Thr Glu  
70 75 80  
gcc ctg cag agc agc cgg aca gag atc acg gag ctc cgc cgc tct gtg 467  
Ala Leu Gln Ser Ser Arg Thr Glu Ile Thr Glu Leu Arg Arg Ser Val  
85 90 95  
cag aac ctg gag att gag ctg cag tcc cag ctc agc atg aaa gca tca 515  
Gln Asn Leu Glu Ile Glu Leu Gln Ser Gln Leu Ser Met Lys Ala Ser  
100 105 110

701049\_sequence\_listing.txt

ctg	gag	aac	agc	ctg	gca	gag	aca	gag	gcg	cgc	tat	ggg	gcc	cag	ctg	563								
Leu	Glu	Asn	Ser	Leu	Ala	Glu	Thr	Glu	Ala	Arg	Tyr	Gly	Ala	Gln	Leu									
	115					120					125													
gcg	cag	ctg	cag	ggc	ctc	att	agc	agt	gtg	gaa	cag	cag	ctg	tgt	gag	611								
Ala	Gln	Leu	Gln	Gly	Leu	Ile	Ser	Ser	Val	Glu	Gln	Gln	Leu	Cys	Glu									
130					135					140					145									
ctg	cgt	tgt	gac	atg	gaa	agg	cag	aat	cat	gag	tac	cag	gtg	ctg	ctg	659								
Leu	Arg	Cys	Asp	Met	Glu	Arg	Gln	Asn	His	Glu	Tyr	Gln	Val	Leu	Leu									
				150					155					160										
gat	gtg	aag	acc	cga	ctg	gag	cag	gag	atc	gcc	acc	tac	cgc	cgt	ctg	707								
Asp	Val	Lys	Thr	Arg	Leu	Glu	Gln	Glu	Ile	Ala	Thr	Tyr	Arg	Arg	Leu									
			165					170					175											
ctg	gag	ggc	gag	gac	gcc	cac	ctg	gct	act	caa	tac	tcc	tca	tcc	ctg	755								
Leu	Glu	Gly	Glu	Asp	Ala	His	Leu	Ala	Thr	Gln	Tyr	Ser	Ser	Ser	Leu									
		180					185					190												
gct	tcg	cag	ccc	tcc	cga	gaa	ggc	atg	gtg	acc	agc	cgc	cag	gtg	cgc	803								
Ala	Ser	Gln	Pro	Ser	Arg	Glu	Gly	Met	Val	Thr	Ser	Arg	Gln	Val	Arg									
	195					200					205													
acc	att	gtg	gag	gaa	gtc	cag	gat	ggc	aag	gtg	ttt	tcc	tcc	aga	gag	851								
Thr	Ile	Val	Glu	Glu	Val	Gln	Asp	Gly	Lys	Val	Phe	Ser	Ser	Arg	Glu									
210					215					220					225									
cag	gag	cac	cgc	tcc	acc	cac	tgaggcccct gtctgcgtat gatagcccag									902								
Gln	Glu	His	Arg	Ser	Thr	His																		
				230																				
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agctgttgcc ttctgtgttt gctttgtgct gccccttaca gagaggcccc ttgggttgac																1022								
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 <212> PRT  
 <213> Mus musculus

<400> 22																
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Asn	Ala	Leu	Arg	Gly	Gln	Val	Gly	Gly	Asp	Val	Asn	Val	Glu	Met	Asp	
			20				25						30			
Ala	Ala	Pro	Gly	Val	Asp	Leu	Ser	Arg	Ile	Leu	Asn	Glu	Met	Arg	Asp	
		35					40					45				
Gln	Tyr	Glu	Lys	Met	Ala	Glu	Lys	Asn	Arg	Lys	Asp	Ala	Glu	Glu	Trp	
	50					55					60					
Phe	Phe	Thr	Lys	Thr	Glu	Glu	Leu	Asn	Arg	Glu	Val	Ala	Thr	Asn	Thr	
65					70					75				80		
Glu	Ala	Leu	Gln	Ser	Ser	Arg	Thr	Glu	Ile	Thr	Glu	Leu	Arg	Arg	Ser	
				85					90					95		



701049\_sequence\_listing.txt

Val Gln Asn Leu Glu Ile Glu Leu Gln Ser Gln Leu Ser Met Lys Ala  
100 105 110  
Ser Leu Glu Asn Ser Leu Ala Glu Thr Glu Ala Arg Tyr Gly Ala Gln  
115 120 125  
Leu Ala Gln Leu Gln Gly Leu Ile Ser Ser Val Glu Gln Gln Leu Cys  
130 135 140  
Glu Leu Arg Cys Asp Met Glu Arg Gln Asn His Glu Tyr Gln Val Leu  
145 150 155 160  
Leu Asp Val Lys Thr Arg Leu Glu Gln Glu Ile Ala Thr Tyr Arg Arg  
165 170 175  
Leu Leu Glu Gly Glu Asp Ala His Leu Ala Thr Gln Tyr Ser Ser Ser  
180 185 190  
Leu Ala Ser Gln Pro Ser Arg Glu Gly Met Val Thr Ser Arg Gln Val  
195 200 205  
Arg Thr Ile Val Glu Glu Val Gln Asp Gly Lys Val Phe Ser Ser Arg  
210 215 220  
Glu Gln Glu His Arg Ser Thr His  
225 230

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<222> (139)..(1401)

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ttctagccga ttacatca atg ggt tcc cgg gag aca cct tct tct tgc tct 171  
Met Gly Ser Arg Glu Thr Pro Ser Ser Cys Ser  
1 5 10  
aag acc ctt gaa acc ttg gac ctg gag act tcc gac agc tct agc cct 219  
Lys Thr Leu Glu Thr Leu Asp Leu Glu Thr Ser Asp Ser Ser Ser Pro  
15 20 25  
gat gct gac agt cct ctg gaa gag caa tgg ctg aaa tcc tcc cca gcc 267  
Asp Ala Asp Ser Pro Leu Glu Glu Gln Trp Leu Lys Ser Ser Pro Ala  
30 35 40  
ctg aag gag gac agt gtg gat gtg gta ctg gaa gac tgc aaa gag cct 315  
Leu Lys Glu Asp Ser Val Asp Val Val Leu Glu Asp Cys Lys Glu Pro  
45 50 55  
ctg tcc ccc tcc tcg cct ccg aca ggc aga gag atg atc agg tac gaa 363  
Leu Ser Pro Ser Ser Pro Pro Thr Gly Arg Glu Met Ile Arg Tyr Glu  
60 65 70 75

## 701049\_sequence\_listing.txt

gtc	aaa	gtg	aac	cga	cgg	agc	att	gaa	gac	atc	tgc	ctc	tgc	tgt	gga	411
Val	Lys	Val	Asn	Arg	Arg	Ser	Ile	Glu	Asp	Ile	Cys	Leu	Cys	Cys	Gly	
				80					85					90		
act	ctc	cag	gtg	tac	act	cgg	cac	ccc	ttg	ttt	gag	gga	ggg	tta	tgt	459
Thr	Leu	Gln	Val	Tyr	Thr	Arg	His	Pro	Leu	Phe	Glu	Gly	Gly	Leu	Cys	
			95					100					105			
gcc	cca	tgt	aag	gat	aag	ttc	ctg	gag	tcc	ctc	ttc	ctg	tat	gat	gat	507
Ala	Pro	Cys	Lys	Asp	Lys	Phe	Leu	Glu	Ser	Leu	Phe	Leu	Tyr	Asp	Asp	
		110					115					120				
gat	gga	cac	cag	agt	tac	tgc	acc	atc	tgc	tgt	tcc	ggg	ggg	acc	ctg	555
Asp	Gly	His	Gln	Ser	Tyr	Cys	Thr	Ile	Cys	Cys	Ser	Gly	Gly	Thr	Leu	
	125					130					135					
ttc	atc	tgt	gag	agc	ccc	gac	tgt	acc	aga	tgc	tac	tgt	ttc	gag	tgt	603
Phe	Ile	Cys	Glu	Ser	Pro	Asp	Cys	Thr	Arg	Cys	Tyr	Cys	Phe	Glu	Cys	
140					145					150					155	
gtg	gac	atc	ctg	gtg	ggc	ccc	ggg	acc	tca	gag	agg	atc	aat	gcc	atg	651
Val	Asp	Ile	Leu	Val	Gly	Pro	Gly	Thr	Ser	Glu	Arg	Ile	Asn	Ala	Met	
				160					165					170		
gcc	tgc	tgg	gtt	tgc	ttc	ctg	tgc	ctg	ccc	ttc	tca	cgg	agt	gga	ctg	699
Ala	Cys	Trp	Val	Cys	Phe	Leu	Cys	Leu	Pro	Phe	Ser	Arg	Ser	Gly	Leu	
			175					180					185			
ctg	cag	agg	cgc	aag	agg	tgg	cgg	cac	cag	ctg	aag	gcc	ttc	cat	gat	747
Leu	Gln	Arg	Arg	Lys	Arg	Trp	Arg	His	Gln	Leu	Lys	Ala	Phe	His	Asp	
		190					195					200				
caa	gag	gga	gcg	ggc	cct	atg	gag	ata	tac	aag	aca	gtg	tct	gca	tgg	795
Gln	Glu	Gly	Ala	Gly	Pro	Met	Glu	Ile	Tyr	Lys	Thr	Val	Ser	Ala	Trp	
	205					210					215					
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Lys	Arg	Gln	Pro	Val	Arg	Val	Leu	Ser	Leu	Phe	Arg	Asn	Ile	Asp	Lys	
220					225					230					235	
gta	cta	aag	agt	ttg	ggc	ttt	ttg	gaa	agc	ggg	tct	ggg	tct	ggg	gga	891
Val	Leu	Lys	Ser	Leu	Gly	Phe	Leu	Glu	Ser	Gly	Ser	Gly	Ser	Gly	Gly	
				240					245					250		
gga	acg	ctg	aag	tac	gtg	gaa	gat	gtc	aca	aat	gtc	gtg	agg	aga	gac	939
Gly	Thr	Leu	Lys	Tyr	Val	Glu	Asp	Val	Thr	Asn	Val	Val	Arg	Arg	Asp	
			255					260					265			
gtg	gag	aaa	tgg	ggc	ccc	ttt	gac	ctg	gtg	tac	ggc	tcg	acg	cag	ccc	987
Val	Glu	Lys	Trp	Gly	Pro	Phe	Asp	Leu	Val	Tyr	Gly	Ser	Thr	Gln	Pro	
		270					275					280				
cta	ggc	agc	tct	tgt	gat	cgc	tgt	ccc	ggc	tgg	tac	atg	ttc	cag	ttc	1035
Leu	Gly	Ser	Ser	Cys	Asp	Arg	Cys	Pro	Gly	Trp	Tyr	Met	Phe	Gln	Phe	
	285					290					295					
cac	cgg	atc	ctg	cag	tat	gcg	ctg	cct	cgc	cag	gag	agt	cag	cgg	ccc	1083
His	Arg	Ile	Leu	Gln	Tyr	Ala	Leu	Pro	Arg	Gln	Glu	Ser	Gln	Arg	Pro	
300					305					310					315	
ttc	ttc	tgg	ata	ttc	atg	gac	aat	ctg	ctg	ctg	act	gag	gat	gac	caa	1131
Phe	Phe	Trp	Ile	Phe	Met	Asp	Asn	Leu	Leu	Leu	Thr	Glu	Asp	Asp	Gln	

## 701049\_sequence\_listing.txt

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320                               325                               330
gag aca act acc cgc ttc ctt cag aca gag gct gtg acc ctc cag gat 1179
Glu Thr Thr Thr Arg Phe Leu Gln Thr Glu Ala Val Thr Leu Gln Asp
335                               340                               345

gtc cgt ggc aga gac tac cag aat gct atg cgg gtg tgg agc aac att 1227
Val Arg Gly Arg Asp Tyr Gln Asn Ala Met Arg Val Trp Ser Asn Ile
350                               355                               360

cca ggg ctg aag agc aag cat gcg ccc ctg acc cca aag gaa gaa gag 1275
Pro Gly Leu Lys Ser Lys His Ala Pro Leu Thr Pro Lys Glu Glu Glu
365                               370                               375

tat ctg caa gcc caa gtc aga agc agg agc aag ctg gac gcc ccg aaa 1323
Tyr Leu Gln Ala Gln Val Arg Ser Arg Ser Lys Leu Asp Ala Pro Lys
380                               385                               390

gtt gac ctc ctg gtg aag aac tgc ctt ctc ccg ctg aga gag tac ttc 1371
Val Asp Leu Leu Val Lys Asn Cys Leu Leu Pro Leu Arg Glu Tyr Phe
400                               405                               410

aag tat ttt tct caa aac tca ctt cct ctt tagaaatgaa tcaccataag 1421
Lys Tyr Phe Ser Gln Asn Ser Leu Pro Leu
415                               420

atgaaagtct ttcctagaac cagggcagat ttcttcctaa ggtctcttcc ctccacagtt 1481
ttctctgggtt tgctttcagg ccttcggggtt tctctcctgt ttgattgccca ggatgcctct 1541
gtgcagctca ctttgcgggg tgggaggtgc ctacggctct gcacaagttc ccggtgggat 1601
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aggattggtt 1670

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 <213> Mus musculus

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Leu Glu Glu Gln Trp Leu Lys Ser Ser Pro Ala Leu Lys Glu Asp Ser
35      40      45
Val Asp Val Val Leu Glu Asp Cys Lys Glu Pro Leu Ser Pro Ser Ser
50      55      60
Pro Pro Thr Gly Arg Glu Met Ile Arg Tyr Glu Val Lys Val Asn Arg
65      70      75      80
Arg Ser Ile Glu Asp Ile Cys Leu Cys Cys Gly Thr Leu Gln Val Tyr
85      90      95
Thr Arg His Pro Leu Phe Glu Gly Gly Leu Cys Ala Pro Cys Lys Asp
100      105      110

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## 701049\_sequence\_listing.txt

Lys Phe Leu Glu Ser Leu Phe Leu Tyr Asp Asp Asp Gly His Gln Ser  
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 Tyr Cys Thr Ile Cys Cys Ser Gly Gly Thr Leu Phe Ile Cys Glu Ser  
 130 135 140  
 Pro Asp Cys Thr Arg Cys Tyr Cys Phe Glu Cys Val Asp Ile Leu Val  
 145 150 155 160  
 Gly Pro Gly Thr Ser Glu Arg Ile Asn Ala Met Ala Cys Trp Val Cys  
 165 170 175  
 Phe Leu Cys Leu Pro Phe Ser Arg Ser Gly Leu Leu Gln Arg Arg Lys  
 180 185 190  
 Arg Trp Arg His Gln Leu Lys Ala Phe His Asp Gln Glu Gly Ala Gly  
 195 200 205  
 Pro Met Glu Ile Tyr Lys Thr Val Ser Ala Trp Lys Arg Gln Pro Val  
 210 215 220  
 Arg Val Leu Ser Leu Phe Arg Asn Ile Asp Lys Val Leu Lys Ser Leu  
 225 230 235 240  
 Gly Phe Leu Glu Ser Gly Ser Gly Ser Gly Gly Gly Thr Leu Lys Tyr  
 245 250 255  
 Val Glu Asp Val Thr Asn Val Val Arg Arg Asp Val Glu Lys Trp Gly  
 260 265 270  
 Pro Phe Asp Leu Val Tyr Gly Ser Thr Gln Pro Leu Gly Ser Ser Cys  
 275 280 285  
 Asp Arg Cys Pro Gly Trp Tyr Met Phe Gln Phe His Arg Ile Leu Gln  
 290 295 300  
 Tyr Ala Leu Pro Arg Gln Glu Ser Gln Arg Pro Phe Phe Trp Ile Phe  
 305 310 315 320  
 Met Asp Asn Leu Leu Leu Thr Glu Asp Asp Gln Glu Thr Thr Thr Arg  
 325 330 335  
 Phe Leu Gln Thr Glu Ala Val Thr Leu Gln Asp Val Arg Gly Arg Asp  
 340 345 350  
 Tyr Gln Asn Ala Met Arg Val Trp Ser Asn Ile Pro Gly Leu Lys Ser  
 355 360 365  
 Lys His Ala Pro Leu Thr Pro Lys Glu Glu Glu Tyr Leu Gln Ala Gln  
 370 375 380  
 Val Arg Ser Arg Ser Lys Leu Asp Ala Pro Lys Val Asp Leu Leu Val  
 385 390 395 400  
 Lys Asn Cys Leu Leu Pro Leu Arg Glu Tyr Phe Lys Tyr Phe Ser Gln  
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 Asn Ser Leu Pro Leu  
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<212> DNA
<213> Homo sapiens
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cc	ct	cccc	ac	ct	gag	gg	gt	tc	ct	tt	cc	ct	g	ccc	gt	cccc	ag	ct	tc	ct	ag	ct	cccc	ac	ccc	180							
ca	ag	t	ga	ccc	ccc	gc	ag	ct	c	tc	g	ccc	ct	c	cc	act	g	ca	aaa	cc	gg	c	act	ga	agg	g	ct	g	ccc	240			
cg	cccc	cg	cc	ct	cccc	cg	cc	cg	c	gg	g	ac	g	ccc	ag	at	tc	tt	tg	cccc	cat	ag	c	ct	tg	g	300						
tg	ac	ct	ct	tg	cc	ac	cc	g	ct	g	tc	g	tc	ag	gt	g	tc	cc	ag	gt	g	gc	ct	tg	g	gc	ct	tt	ct	tt	tg	cc	360
gc	gc	cg	gt	ccc	tc	gt	tt	cc	at	g	ccc	ag	tc	ct	ccc	cg	gg	g	ac	ct	g	c	ct	g	ag	cc	cc	cg	g	420			
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	1				5					10																							
gac	gtg	att	ttg	gtg	gga	tcc	agt	gag	ctc	tca	agc	tcc	gtt	tca	ccc	577																	
Asp	Val	Ile	Leu	Val	Gly	Ser	Ser	Glu	Leu	Ser	Ser	Ser	Val	Ser	Pro	30																	
				20					25					30																			
ggg	aca	ggc	aga	gat	ctt	att	gca	tat	gaa	gtc	aag	gct	aac	cag	cga	625																	
Gly	Thr	Gly	Arg	Asp	Leu	Ile	Ala	Tyr	Glu	Val	Lys	Ala	Asn	Gln	Arg	45																	
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aat	ata	gaa	gac	atc	tgc	atc	tgc	tgc	gga	agt	ctc	cag	gtt	cac	aca	673																	
Asn	Ile	Glu	Asp	Ile	Cys	Ile	Cys	Cys	Gly	Ser	Leu	Gln	Val	His	Thr	60																	
		50					55					60																					
cag	cac	cct	ctg	ttt	gag	gga	ggg	atc	tgc	gcc	cca	tgt	aag	gac	aag	721																	
Gln	His	Pro	Leu	Phe	Glu	Gly	Gly	Ile	Cys	Ala	Pro	Cys	Lys	Asp	Lys	75																	
		65				70					75																						
ttc	ctg	gat	gcc	ctc	ttc	ctg	tac	gac	gat	gac	ggg	tac	caa	tcc	tac	769																	
Phe	Leu	Asp	Ala	Leu	Phe	Leu	Tyr	Asp	Asp	Asp	Gly	Tyr	Gln	Ser	Tyr	95																	
					85					90																							
tgc	tcc	atc	tgc	tgc	tcc	gga	gag	acg	ctg	ctc	atc	tgc	gga	aac	cct	817																	
Cys	Ser	Ile	Cys	Cys	Ser	Gly	Glu	Thr	Leu	Leu	Ile	Cys	Gly	Asn	Pro	100																	
				100					105					110																			
gat	tgc	acc	cga	tgc	tac	tgc	ttc	gag	tgt	gtg	gat	agc	ctg	gtc	ggc	865																	
Asp	Cys	Thr	Arg	Cys	Tyr	Cys	Phe	Glu	Cys	Val	Asp	Ser	Leu	Val	Gly	115																	
			115					120					125																				
ccc	ggg	acc	tcg	ggg	aag	gtg	cac	gcc	atg	agc	aac	tgg	gtg	tgc	tac	913																	
Pro	Gly	Thr	Ser	Gly	Lys	Val	His	Ala	Met	Ser	Asn	Trp	Val	Cys	T																		

## 701049\_sequence\_listing.txt

Leu	Cys	Leu	Pro	Ser	Ser	Arg	Ser	Gly	Leu	Leu	Gln	Arg	Arg	Arg	Lys	
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Trp	Arg	Ser	Gln	Leu	Lys	Ala	Phe	Tyr	Asp	Arg	Glu	Ser	Glu	Asn	Pro	
160					165					170					175	
ctt	gag	atg	ttc	gaa	acc	gtg	cct	gtg	tgg	agg	aga	cag	cca	gtc	cgg	1057
Leu	Glu	Met	Phe	Glu	Thr	Val	Pro	Val	Trp	Arg	Arg	Gln	Pro	Val	Arg	
				180					185					190		
gtg	ctg	tcc	ctt	ttt	gaa	gac	atc	aag	aaa	gag	ctg	acg	agt	ttg	ggc	1105
Val	Leu	Ser	Leu	Phe	Glu	Asp	Ile	Lys	Lys	Glu	Leu	Thr	Ser	Leu	Gly	
			195					200					205			
ttt	ttg	gaa	agt	ggc	tct	gac	ccg	gga	caa	ctg	aag	cat	gtg	gtt	gat	1153
Phe	Leu	Glu	Ser	Gly	Ser	Asp	Pro	Gly	Gln	Leu	Lys	His	Val	Val	Asp	
		210					215					220				
gtc	aca	gac	aca	gtg	agg	aag	gat	gtg	gag	gag	tgg	gga	ccc	ttc	gat	1201
Val	Thr	Asp	Thr	Val	Arg	Lys	Asp	Val	Glu	Glu	Trp	Gly	Pro	Phe	Asp	
	225					230					235					
ctt	gtg	tac	ggc	gcc	aca	gct	ccc	ctg	ggc	cac	acc	tgt	gac	cgt	cct	1249
Leu	Val	Tyr	Gly	Ala	Thr	Ala	Pro	Leu	Gly	His	Thr	Cys	Asp	Arg	Pro	
240				245						250					255	
ccc	agc	tgg	tac	ctg	ttc	cag	ttc	cac	cgg	ttc	ctg	cag	tac	gca	cgg	1297
Pro	Ser	Trp	Tyr	Leu	Phe	Gln	Phe	His	Arg	Phe	Leu	Gln	Tyr	Ala	Arg	
				260					265					270		
ccc	aag	cca	ggc	agc	ccc	agg	ccc	ttc	ttc	tgg	atg	ttc	gtg	gac	aat	1345
Pro	Lys	Pro	Gly	Ser	Pro	Arg	Pro	Phe	Phe	Trp	Met	Phe	Val	Asp	Asn	
			275					280					285			
ctg	gtg	ctg	aac	aag	gaa	gac	ctg	gac	gtc	gca	tct	cgc	ttc	ctg	gag	1393
Leu	Val	Leu	Asn	Lys	Glu	Asp	Leu	Asp	Val	Ala	Ser	Arg	Phe	Leu	Glu	
		290					295					300				
atg	gag	cca	gtc	acc	atc	cca	gat	gtc	cac	ggc	gga	tcc	ttg	cag	aat	1441
Met	Glu	Pro	Val	Thr	Ile	Pro	Asp	Val	His	Gly	Gly	Ser	Leu	Gln	Asn	
	305					310					315					
gct	gtc	cgc	gtg	tgg	agc	aac	atc	cca	gcc	ata	agg	agc	agc	agg	cac	1489
Ala	Val	Arg	Val	Trp	Ser	Asn	Ile	Pro	Ala	Ile	Arg	Ser	Ser	Arg	His	
320				325						330					335	
tgg	gct	ctg	gtt	tcg	gaa	gaa	gaa	ttg	tcc	ctg	ctg	gcc	cag	aac	aag	1537
Trp	Ala	Leu	Val	Ser	Glu	Glu	Glu	Leu	Ser	Leu	Leu	Ala	Gln	Asn	Lys	
				340				345						350		
cag	agc	tcg	aag	ctc	gcg	gcc	aag	tgg	ccc	acc	aag	ctg	gtg	aag	aac	1585
Gln	Ser	Ser	Lys	Leu	Ala	Ala	Lys	Trp	Pro	Thr	Lys	Leu	Val	Lys	Asn	
			355					360					365			
tgc	ttt	ctc	ccc	cta	aga	gaa	tat	ttc	aag	tat	ttt	tca	aca	gaa	ctc	1633
Cys	Phe	Leu	Pro	Leu	Arg	Glu	Tyr	Phe	Lys	Tyr	Phe	Ser	Thr	Glu	Leu	
		370					375					380				
act	tcc	tct	tta	taa	atg	agtc	act	tact	gt	ga	agaaaa	ag	act	ttttc	ccta	1685
Thr	Ser	Ser	Leu													
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gaacaaaggc aactttcctc

1705

&lt;210&gt; 26

&lt;211&gt; 387

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 26

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1 5 10 15Val Ile Leu Val Gly Ser Ser Glu Leu Ser Ser Ser Val Ser Pro Gly  
20 25 30Thr Gly Arg Asp Leu Ile Ala Tyr Glu Val Lys Ala Asn Gln Arg Asn  
35 40 45Ile Glu Asp Ile Cys Ile Cys Cys Gly Ser Leu Gln Val His Thr Gln  
50 55 60His Pro Leu Phe Glu Gly Gly Ile Cys Ala Pro Cys Lys Asp Lys Phe  
65 70 75 80Leu Asp Ala Leu Phe Leu Tyr Asp Asp Asp Gly Tyr Gln Ser Tyr Cys  
85 90 95Ser Ile Cys Cys Ser Gly Glu Thr Leu Leu Ile Cys Gly Asn Pro Asp  
100 105 110Cys Thr Arg Cys Tyr Cys Phe Glu Cys Val Asp Ser Leu Val Gly Pro  
115 120 125Gly Thr Ser Gly Lys Val His Ala Met Ser Asn Trp Val Cys Tyr Leu  
130 135 140Cys Leu Pro Ser Ser Arg Ser Gly Leu Leu Gln Arg Arg Arg Lys Trp  
145 150 155 160Arg Ser Gln Leu Lys Ala Phe Tyr Asp Arg Glu Ser Glu Asn Pro Leu  
165 170 175Glu Met Phe Glu Thr Val Pro Val Trp Arg Arg Gln Pro Val Arg Val  
180 185 190Leu Ser Leu Phe Glu Asp Ile Lys Lys Glu Leu Thr Ser Leu Gly Phe  
195 200 205Leu Glu Ser Gly Ser Asp Pro Gly Gln Leu Lys His Val Val Asp Val  
210 215 220Thr Asp Thr Val Arg Lys Asp Val Glu Glu Trp Gly Pro Phe Asp Leu  
225 230 235 240Val Tyr Gly Ala Thr Ala Pro Leu Gly His Thr Cys Asp Arg Pro Pro  
245 250 255Ser Trp Tyr Leu Phe Gln Phe His Arg Phe Leu Gln Tyr Ala Arg Pro  
260 265 270Lys Pro Gly Ser Pro Arg Pro Phe Phe Trp Met Phe Val Asp Asn Leu  
275 280 285



[illegible]

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<212> DNA
<213> Mus musculus
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<221> CDS
<222> (147) .. (1367)
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atctcctctg tgagagaagg gccagg atg ttc gag gtc ctg gtg ctg aag att															173
Met Phe Glu Val Leu Val Leu Lys Ile															
gaa gat cca ggt tgc ttc tgg gta att ata aaa gga tgt agt cat ttt															221
Glu Asp Pro Gly Cys Phe Trp Val Ile Ile Lys Gly Cys Ser His Phe															
10 15 20 25															
tta gaa caa gaa gtt gac tac caa aaa cta aac act gcc atg aat gac															269
Leu Glu Gln Glu Val Asp Tyr Gln Lys Leu Asn Thr Ala Met Asn Asp															
30 35 40															
ttc tat aac agc atg tgt cag gac gta gaa atg aaa cca tta atg ctg															317
Phe Tyr Asn Ser Met Cys Gln Asp Val Glu Met Lys Pro Leu Met Leu															
45 50 55															
gaa gaa ggg cag gtg tgt gtg gtg tac tgc cag gag ctg aag tgc tgg															365
Glu Glu Gly Gln Val Cys Val Val Tyr Cys Gln Glu Leu Lys Cys Trp															
60 65 70															
tgc agg gct ctg att aag tcc atc atc tct tct gca gac cat tac ctg															413
Cys Arg Ala Leu Ile Lys Ser Ile Ile Ser Ser Ala Asp His Tyr Leu															
75 80 85															
gca gag tgt ttc ctg gtc gat ttt gcc aag tat att cca gta aaa tct															461
Ala Glu Cys Phe Leu Val Asp Phe Ala Lys Tyr Ile Pro Val Lys Ser															

## 701049\_sequence\_listing.txt

90		95		100		105	
aaa Lys	aac Asn	atc Ile	cga Arg	ggt Val 110	gca Ala	gta Val	509
gca Ala	aaa Lys	aaa Lys	ttc Phe 125	aga Arg	ctt Leu	tac Tyr 120	557
gac Asp	ttc Phe	tgt Cys 140	gaa Glu	gac Asp	aat Asn	gct Ala 145	605
agt Ser	gca Ala 155	gcc Ala	atc Ile	cag Gln	tac Tyr	ttt Phe 160	653
gtg Val 170	gaa Glu	gca Ala	aaa Lys	cta Leu	tgt Cys 175	gcg Ala	701
ctt Leu	tat Tyr	gca Ala	aca Thr	ata Ile 190	aaa Lys	aat Asn	749
gtt Val	gca Ala	aag Lys	aat Asn 205	ttt Phe	gct Ala	tat Tyr	797
ctc Leu	aat Asn	cct Pro 220	ttg Leu	gag Glu	aaa Lys	ccc Pro 225	845
tcc Ser	agt Ser 235	aag Lys	ctc Leu	agc Ser	cca Pro	tca Ser 240	893
gga Gly 250	aaa Lys	gac Asp	tat Tyr	cac His	aga Arg 255	atg Met	941
tcc Ser	ttg Leu	aca Thr	gac Asp	tcg Ser 270	cct Pro	aaa Lys	989
ctc Leu	cct Pro	tta Leu	aag Lys 285	cac His	acg Thr	gag Glu	1037
cca Pro	acc Thr	aaa Lys 300	aga Arg	ggc Gly	ata Ile	acc Thr	1085
gta Val	agt Ser 315	ggg Gly	tct Ser	agc Ser	cag Gln	agg Arg 320	1133
gaa Glu 330	aag Lys	aaa Lys	gac Asp	tgt Cys	gac Asp 335	gag Glu	1181
ttt Leu	cta Leu	aat Leu	cct Leu	gat Leu	cct Leu	ttg Leu	1229

## 701049\_sequence\_listing.txt

Phe Leu Asn Pro Asp Pro Leu Arg Ala Asp Gly Thr Ser Asp Leu His  
 350 355 360  
 cag ttg cag aag gtg aag ctg ggc aca ctg cag cct ggg gtg gtg ctc 1277  
 Gln Leu Gln Lys Val Lys Leu Gly Thr Leu Gln Pro Gly Val Val Leu  
 365 370 375  
 cgg aac agg atc gag ccc tgc cta acc ctg gag aaa tca cct ctg tcg 1325  
 Arg Asn Arg Ile Glu Pro Cys Leu Thr Leu Glu Lys Ser Pro Leu Ser  
 380 385 390  
 gca gac ctg aag aag gtg aac atg ttc tta aag cca gac tcc 1367  
 Ala Asp Leu Lys Lys Val Asn Met Phe Leu Lys Pro Asp Ser  
 395 400 405  
 tgacgacatg ccagcccttt ccaacacaga gtgttgcttt gttttgcttt gtctgttctg 1427  
 ttctaagagt gacggggatg aaatacaggg ctttgcgcgt cctggggcatg cattcatcac 1487  
 tgaaccatac cccaattcca taggaggatt ttaaataaac acttctaagg ctacattgca 1547  
 gaattcttgc tcc 1560

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 <212> PRT  
 <213> Mus musculus

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 20 25 30  
 Gln Lys Leu Asn Thr Ala Met Asn Asp Phe Tyr Asn Ser Met Cys Gln  
 35 40 45  
 Asp Val Glu Met Lys Pro Leu Met Leu Glu Glu Gly Gln Val Cys Val  
 50 55 60  
 Val Tyr Cys Gln Glu Leu Lys Cys Trp Cys Arg Ala Leu Ile Lys Ser  
 65 70 75 80  
 Ile Ile Ser Ser Ala Asp His Tyr Leu Ala Glu Cys Phe Leu Val Asp  
 85 90 95  
 Phe Ala Lys Tyr Ile Pro Val Lys Ser Lys Asn Ile Arg Val Ala Val  
 100 105 110  
 Glu Ser Phe Met Gln Leu Pro Tyr Arg Ala Lys Lys Phe Arg Leu Tyr  
 115 120 125  
 Gly Thr Lys Pro Val Thr Leu His Ile Asp Phe Cys Glu Asp Asn Ala  
 130 135 140  
 Glu Ile Val Pro Ala Thr Lys Trp Asp Ser Ala Ala Ile Gln Tyr Phe  
 145 150 155 160  
 Gln Asn Leu Leu Arg Ala Thr Thr Gln Val Glu Ala Lys Leu Cys Ala  
 165 170 175

## 701049\_sequence\_listing.txt

Val Glu Glu Asp Thr Phe Glu Val Tyr Leu Tyr Ala Thr Ile Lys Asn  
 180 185 190  
 Glu Lys Val Cys Val Asn Asp Asp Leu Val Ala Lys Asn Phe Ala Tyr  
 195 200 205  
 Tyr Val Ser Pro Met Gly Asn Lys Asn Leu Asn Pro Leu Glu Lys Pro  
 210 215 220  
 Arg Gln Ser Leu Asn Ser Val Thr Cys Ser Ser Lys Leu Ser Pro Ser  
 225 230 235 240  
 Leu Thr Leu Trp Pro Met Leu Leu Gln Gly Lys Asp Tyr His Arg Met  
 245 250 255  
 Glu Asn Lys Ala Leu Asn Tyr Lys Asp Ser Leu Thr Asp Ser Pro Lys  
 260 265 270  
 Met Met Leu Glu Lys Gln Gln Gln Ser Leu Pro Leu Lys His Thr Glu  
 275 280 285  
 Lys Cys Thr Glu Ser Ser Val Tyr Trp Pro Thr Lys Arg Gly Ile Thr  
 290 295 300  
 Ile Tyr Ala Asp Pro Asp Val Pro Ser Val Ser Gly Ser Ser Gln Arg  
 305 310 315 320  
 Pro Asn Glu Lys Pro Leu Arg Leu Thr Glu Lys Lys Asp Cys Asp Glu  
 325 330 335  
 Lys Asn Gly Cys Val Lys Leu Leu Gln Phe Leu Asn Pro Asp Pro Leu  
 340 345 350  
 Arg Ala Asp Gly Thr Ser Asp Leu His Gln Leu Gln Lys Val Lys Leu  
 355 360 365  
 Gly Thr Leu Gln Pro Gly Val Val Leu Arg Asn Arg Ile Glu Pro Cys  
 370 375 380  
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 385 390 395 400  
 Met Phe Leu Lys Pro Asp Ser  
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<210> 29  
 <211> 1301  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (97)..(1167)

<400> 29  
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 gatcatgatg tcgattatca aaaattaaat agtgcc atg aat gac ttc tac aac 114  
 Met Asn Asp Phe Tyr Asn  
 1 5

## 701049\_sequence\_listing.txt

agc Ser	acg Thr	tgt Cys	caa Gln 10	gat Asp	ata Ile	gaa Glu	ata Ile	aaa Lys 15	ccc Pro	tta Leu	aca Thr	ttg Leu	gaa Glu 20	gaa Glu	gga Gly	162
cag Gln	gtg Val	tgt Cys 25	gtg Val	gtc Val	tat Tyr	tgt Cys	gag Glu 30	gag Glu	cta Leu	aag Lys	tgc Cys	tgg Trp 35	tgc Cys	agg Arg	gcc Ala	210
att Ile	gtc Val 40	aaa Lys	tca Ser	att Ile	acg Thr	tct Ser 45	tcc Ser	gca Ala	gac Asp	cag Gln	tac Tyr 50	ctg Leu	gca Ala	gaa Glu	tgt Cys	258
ttc Phe 55	ctt Leu	gtg Val	gac Asp	ttt Phe	gcc Ala 60	aag Lys	aac Asn	att Ile	cca Pro	gtc Val 65	aaa Lys	tct Ser	aaa Lys	agc Ser	atc Ile 70	306
cga Arg	gtt Val	gta Val	gta Val	gaa Glu 75	tcg Ser	ttt Phe	atg Met	cag Gln	ctt Leu 80	ccc Pro	tat Tyr	aga Arg	gca Ala	aaa Lys 85	aaa Lys	354
ttc Phe	agc Ser	ctg Leu	tac Tyr 90	tgc Cys	aca Thr	aag Lys	cct Pro	gtc Val 95	aca Thr	tta Leu	cac His	att Ile	gac Asp 100	ttc Phe	tgc Cys	402
cga Arg	gac Asp	agt Ser 105	act Thr	gac Asp	att Ile	gtg Val	cct Pro 110	gcc Ala	aag Lys	aag Lys	tgg Trp	gac Asp 115	aat Asn	gca Ala	gct Ala	450
att Ile	cag Gln 120	tac Tyr	ttt Phe	cag Gln	aac Asn	ctt Leu 125	ctg Leu	aaa Lys	gca Ala	act Thr	acc Thr 130	cag Gln	gtg Val	gaa Glu	gcc Ala	498
aga Arg 135	tta Leu	tgt Cys	gct Ala	gtg Val	gaa Glu 140	gaa Glu	gat Asp	aca Thr	ttt Phe	gag Glu 145	gtt Val	tac Tyr	ctt Leu	tat Tyr	gta Val 150	546
act Thr	ata Ile	aaa Lys	gat Asp	gaa Glu 155	aaa Lys	gtt Val	tgt Cys	gtt Val	aat Asn 160	gat Asp	gat Asp	ctt Leu	gtt Val	gca Ala 165	aag Lys	594
aac Asn	tat Tyr	gct Ala	tgt Cys 170	tat Tyr	atg Met	tca Ser	cct Pro	aca Thr 175	aag Lys	aat Asn	aaa Lys	aac Asn	ctt Leu 180	gat Asp	tat Tyr	642
tta Leu	gaa Glu 185	aaa Lys	cca Pro	aga Arg	ttg Leu	aat Asn	ata Ile 190	aaa Lys	tca Ser	gca Ala	ccc Pro	tcc Ser 195	ttc Phe	aat Asn	aaa Lys	690
ctc Leu	aat Asn 200	cca Pro	gca Ala	ctt Leu	aca Thr	ctc Leu 205	tgg Trp	cca Pro	atg Met	ttt Phe	ttg Leu 210	caa Gln	gga Gly	aaa Lys	gat Asp	738
gtt Val 215	caa Gln	gga Gly	atg Met	gaa Glu	gat Asp 220	tca Ser	cat His	ggg Gly	gta Val	aat Asn 225	ttt Phe	ccg Pro	gca Ala	caa Gln	tct Ser 230	786
ctg Leu	caa Gln	cat His	aca Thr	tgg Trp 235	tgc Cys	aag Lys	ggg Gly	att Ile	gtc Val 240	ggg Gly	gac Asp	ctc Leu	agg Arg	cca Pro 245	aca Thr	834
gcc Ala	aca Thr	gca Ala	cag Gln 250	gac Asp	aaa Lys	gct Ala	gta Val	aaa Lys 255	tgt Cys	aat Asn	atg Met	gat Asp	tca Ser 260	ttg Leu	aga Arg	882

701049\_sequence\_listing.txt

gat	tca	cct	aaa	gac	aaa	tct	gaa	aag	aaa	cac	cat	tgc	atc	tct	tta	930
Asp	Ser	Pro	Lys	Asp	Lys	Ser	Glu	Lys	Lys	His	His	Cys	Ile	Ser	Leu	
		265					270					275				
aaa	gat	aca	aat	aag	cgt	gtt	gaa	tcc	tca	gtg	tac	tgg	cca	gca	aaa	978
Lys	Asp	Thr	Asn	Lys	Arg	Val	Glu	Ser	Ser	Val	Tyr	Trp	Pro	Ala	Lys	
	280					285					290					
aga	ggc	ata	acc	ata	tat	gct	gat	cca	gat	gta	cca	gaa	gca	agt	gct	1026
Arg	Gly	Ile	Thr	Ile	Tyr	Ala	Asp	Pro	Asp	Val	Pro	Glu	Ala	Ser	Ala	
295					300					305					310	
tta	agt	cag	aag	tca	aat	gag	aaa	cct	ctt	aga	ttg	act	gag	aag	aaa	1074
Leu	Ser	Gln	Lys	Ser	Asn	Glu	Lys	Pro	Leu	Arg	Leu	Thr	Glu	Lys	Lys	
				315					320					325		
gaa	tat	gat	gag	aag	aat	agc	tgt	gtg	aaa	tta	ctg	cag	ttt	tta	aat	1122
Glu	Tyr	Asp	Glu	Lys	Asn	Ser	Cys	Val	Lys	Leu	Leu	Gln	Phe	Leu	Asn	
			330					335					340			
cct	gat	cct	ttg	aga	gct	gac	gga	atc	tct	gat	ctc	cag	cag	act		1167
Pro	Asp	Pro	Leu	Arg	Ala	Asp	Gly	Ile	Ser	Asp	Leu	Gln	Gln	Thr		
		345					350					355				
tgagattaga	agagaaactc	cttagatggg	ggacttaacc	tgaagacatc	cttttagaaa											1227
cgatcgaatg	gattgttgct	tctgagaaat	tgttccttgt	tttttggata	ataaacgatc											1287
ttccttttgg	taaa															1301

<210> 30  
 <211> 357  
 <212> PRT  
 <213> Homo sapiens

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Leu	Thr	Leu	Glu	Glu	Gly	Gln	Val	Cys	Val	Val	Tyr	Cys	Glu	Glu	Leu		
			20					25					30				
Lys	Cys	Trp	Cys	Arg	Ala	Ile	Val	Lys	Ser	Ile	Thr	Ser	Ser	Ala	Asp		
		35					40					45					
Gln	Tyr	Leu	Ala	Glu	Cys	Phe	Leu	Val	Asp	Phe	Ala	Lys	Asn	Ile	Pro		
	50					55					60						
Val	Lys	Ser	Lys	Ser	Ile	Arg	Val	Val	Val	Glu	Ser	Phe	Met	Gln	Leu		
	65				70					75					80		
Pro	Tyr	Arg	Ala	Lys	Lys	Phe	Ser	Leu	Tyr	Cys	Thr	Lys	Pro	Val	Thr		
				85					90					95			
Leu	His	Ile	Asp	Phe	Cys	Arg	Asp	Ser	Thr	Asp	Ile	Val	Pro	Ala	Lys		
			100					105					110				
Lys	Trp	Asp	Asn	Ala	Ala	Ile	Gln	Tyr	Phe	Gln	Asn	Leu	Leu	Lys	Ala		
		115					120					125					
Thr	Thr	Gln	Val	Glu	Ala	Arg	Leu	Cys	Ala	Val	Glu	Glu	Asp	Thr	Phe		

## 701049\_sequence\_listing.txt

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130                               135                               140
Glu Val Tyr Leu Tyr Val Thr Ile Lys Asp Glu Lys Val Cys Val Asn
145                               150                               155                               160
Asp Asp Leu Val Ala Lys Asn Tyr Ala Cys Tyr Met Ser Pro Thr Lys
165                               170                               175
Asn Lys Asn Leu Asp Tyr Leu Glu Lys Pro Arg Leu Asn Ile Lys Ser
180                               185                               190
Ala Pro Ser Phe Asn Lys Leu Asn Pro Ala Leu Thr Leu Trp Pro Met
195                               200                               205
Phe Leu Gln Gly Lys Asp Val Gln Gly Met Glu Asp Ser His Gly Val
210                               215                               220
Asn Phe Pro Ala Gln Ser Leu Gln His Thr Trp Cys Lys Gly Ile Val
225                               230                               235
Gly Asp Leu Arg Pro Thr Ala Thr Ala Gln Asp Lys Ala Val Lys Cys
245                               250                               255
Asn Met Asp Ser Leu Arg Asp Ser Pro Lys Asp Lys Ser Glu Lys Lys
260                               265                               270
His His Cys Ile Ser Leu Lys Asp Thr Asn Lys Arg Val Glu Ser Ser
275                               280                               285
Val Tyr Trp Pro Ala Lys Arg Gly Ile Thr Ile Tyr Ala Asp Pro Asp
290                               295                               300
Val Pro Glu Ala Ser Ala Leu Ser Gln Lys Ser Asn Glu Lys Pro Leu
305                               310                               315
Arg Leu Thr Glu Lys Lys Glu Tyr Asp Glu Lys Asn Ser Cys Val Lys
325                               330                               335
Leu Leu Gln Phe Leu Asn Pro Asp Pro Leu Arg Ala Asp Gly Ile Ser
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Asp Leu Gln Gln Thr
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<210> 31
<211> 1280
<212> DNA
<213> Mus musculus

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<222> (122)..(1219)

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c atg cag cct tat caa cgg ctt ctg gcg ctt ggc ttc ctt ctg tta acc 169
Met Gln Pro Tyr Gln Arg Leu Leu Ala Leu Gly Phe Leu Leu Leu Thr
1 5 10 15

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## 701049\_sequence\_listing.txt

ctg	ccc	tgg	ggc	cag	aca	tcc	gag	ttt	caa	gac	tct	gac	ctt	ttg	cag	217
Leu	Pro	Trp	Gly 20	Gln	Thr	Ser	Glu	Phe 25	Gln	Asp	Ser	Asp	Leu 30	Leu	Gln	
ttt	ctg	gga	tta	gag	aaa	gcg	cct	tca	cct	cac	agg	ttc	caa	cct	gtg	265
Phe	Leu	Gly 35	Leu	Glu	Lys	Ala	Pro 40	Ser	Pro	His	Arg	Phe 45	Gln	Pro	Val	
cct	cgc	gtc	tta	agg	aaa	atc	atc	cgg	gct	cga	gaa	gcc	gct	gca	gcc	313
Pro	Arg 50	Val	Leu	Arg	Lys	Ile 55	Ile	Arg	Ala	Arg	Glu 60	Ala	Ala	Ala	Ala	
agt	ggg	gcc	tcg	cag	gac	tta	tgc	tac	gtg	aag	gag	ctg	ggg	gtt	cgt	361
Ser 65	Gly	Ala	Ser	Gln	Asp 70	Leu	Cys	Tyr	Val	Lys 75	Glu	Leu	Gly	Val	Arg 80	
ggg	aac	ctg	ctt	cag	ctt	ctc	cca	gac	cag	ggg	ttt	ttc	ctt	aat	aca	409
Gly	Asn	Leu	Leu	Gln 85	Leu	Leu	Pro	Asp	Gln 90	Gly	Phe	Phe	Leu	Asn 95	Thr	
cag	aaa	cct	ttc	caa	gat	ggc	tcc	tgt	ctc	cag	aag	gtc	ctc	tat	ttt	457
Gln	Lys	Pro	Phe 100	Gln	Asp	Gly	Ser	Cys 105	Leu	Gln	Lys	Val	Leu 110	Tyr	Phe	
aac	ttg	tct	gcc	atc	aaa	gaa	aag	gca	aag	ttg	acc	atg	gcc	cag	ctg	505
Asn	Leu	Ser 115	Ala	Ile	Lys	Glu	Lys 120	Ala	Lys	Leu	Thr	Met 125	Ala	Gln	Leu	
act	cta	gac	ttg	ggg	ccc	agg	tcc	tac	tat	aac	ctg	cga	cca	gag	ctg	553
Thr	Leu 130	Asp	Leu	Gly	Pro	Arg 135	Ser	Tyr	Tyr	Asn	Leu 140	Arg	Pro	Glu	Leu	
gtg	gtt	gct	ctg	tct	gtg	gtt	cag	gac	cgg	ggc	gtg	tgg	ggg	cga	tcc	601
Val 145	Val	Ala	Leu	Ser	Val 150	Val	Gln	Asp	Arg	Gly 155	Val	Trp	Gly	Arg	Ser 160	
cac	cct	aag	gtg	ggc	aga	ttg	ctt	ttt	ctg	cgg	tct	gtc	cct	ggg	cct	649
His	Pro	Lys	Val	Gly 165	Arg	Leu	Leu	Phe	Leu 170	Arg	Ser	Val	Pro	Gly 175	Pro	
caa	ggg	cag	ctc	cag	ttc	aac	ctg	cag	ggg	gcg	ctt	aag	gat	tgg	agc	697
Gln	Gly	Gln	Leu 180	Gln	Phe	Asn	Leu	Gln 185	Gly	Ala	Leu	Lys	Asp 190	Trp	Ser	
agc	aac	cga	ctg	aag	aat	ttg	gac	tta	cac	tta	gag	att	ttg	gtc	aaa	745
Ser	Asn	Arg 195	Leu	Lys	Asn	Leu	Asp 200	Leu	His	Leu	Glu	Ile 205	Leu	Val	Lys	
gag	gac	aga	tac	tcc	agg	gta	act	gtc	cag	ccc	gag	aac	ccc	tgt	gac	793
Glu	Asp 210	Arg	Tyr	Ser	Arg	Val 215	Thr	Val	Gln	Pro	Glu 220	Asn	Pro	Cys	Asp	
ccg	ctg	ctc	cgc	tct	cta	cat	gcc	tcg	ctg	ctg	gtg	gta	acc	ctc	aat	841
Pro 225	Leu	Leu	Arg	Ser	Leu 230	His	Ala	Ser	Leu	Leu 235	Val	Val	Thr	Leu	Asn 240	
cct	aaa	cac	tgt	cat	cct	tct	tcc	aga	aaa	agg	agg	gcg	gcc	atc	tct	889
Pro	Lys	His	Cys	His 245	Pro	Ser	Ser	Arg	Lys 250	Arg	Arg	Ala	Ala	Ile 255	Ser	
gtc	ccc	aag	ggg	ttc	tgt	agg	aac	ttc	tgc	cac	cgt	cat	cag	ctg	ttc	937
Val	Pro	Lys	Gly	Phe	Cys	Arg	Asn	Phe	Cys	His	Arg	His	Gln	Leu	Phe	

## 701049\_sequence\_listing.txt

260

265

270

```

atc aac ttc cag gac ctg ggt tgg cac aag tgg gtc atc gcc cct aag 985
Ile Asn Phe Gln Asp Leu Gly Trp His Lys Trp Val Ile Ala Pro Lys
275 280 285

ggg ttc atg gca aat tac tgt cat gga gag tgc ccc ttc tca atg acc 1033
Gly Phe Met Ala Asn Tyr Cys His Gly Glu Cys Pro Phe Ser Met Thr
290 295 300

acg tat tta aat agt tcc aat tat gct ttc atg cag gct ctg atg cat 1081
Thr Tyr Leu Asn Ser Ser Asn Tyr Ala Phe Met Gln Ala Leu Met His
305 310 315

atg gct gac ccc aag gtc ccc aag gct gtc tgt gtc ccc acc aag ctc 1129
Met Ala Asp Pro Lys Val Pro Lys Ala Val Cys Val Pro Thr Lys Leu
325 330 335

tcg ccc atc tcc atg ctc tat cag gat agt gat aag aac gtc att ctc 1177
Ser Pro Ile Ser Met Leu Tyr Gln Asp Ser Asp Lys Asn Val Ile Leu
340 345 350

cga cat tat gaa gac atg gta gtc gat gag tgt ggg tgt ggg 1219
Arg His Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Gly
355 360 365

tagtctcggg actaggctag gagtgtgctt agggtaaadc ctttaataaaa actaccaccc 1279
c 1280

```

```

<210> 32
<211> 366
<212> PRT
<213> Mus musculus

```

```

<400> 32
Met Gln Pro Tyr Gln Arg Leu Leu Ala Leu Gly Phe Leu Leu Leu Thr
1 5 10 15

Leu Pro Trp Gly Gln Thr Ser Glu Phe Gln Asp Ser Asp Leu Leu Gln
20 25 30

Phe Leu Gly Leu Glu Lys Ala Pro Ser Pro His Arg Phe Gln Pro Val
35 40 45

Pro Arg Val Leu Arg Lys Ile Ile Arg Ala Arg Glu Ala Ala Ala Ala
50 55 60

Ser Gly Ala Ser Gln Asp Leu Cys Tyr Val Lys Glu Leu Gly Val Arg
65 70 75 80

Gly Asn Leu Leu Gln Leu Leu Pro Asp Gln Gly Phe Phe Leu Asn Thr
85 90 95

Gln Lys Pro Phe Gln Asp Gly Ser Cys Leu Gln Lys Val Leu Tyr Phe
100 105 110

Asn Leu Ser Ala Ile Lys Glu Lys Ala Lys Leu Thr Met Ala Gln Leu
115 120 125

Thr Leu Asp Leu Gly Pro Arg Ser Tyr Tyr Asn Leu Arg Pro Glu Leu
130 135 140

```

## 701049\_sequence\_listing.txt

```

Val Val Ala Leu Ser Val Val Gln Asp Arg Gly Val Trp Gly Arg Ser
145      150      155      160
His Pro Lys Val Gly Arg Leu Leu Phe Leu Arg Ser Val Pro Gly Pro
      165      170      175
Gln Gly Gln Leu Gln Phe Asn Leu Gln Gly Ala Leu Lys Asp Trp Ser
      180      185      190
Ser Asn Arg Leu Lys Asn Leu Asp Leu His Leu Glu Ile Leu Val Lys
      195      200      205
Glu Asp Arg Tyr Ser Arg Val Thr Val Gln Pro Glu Asn Pro Cys Asp
      210      215      220
Pro Leu Leu Arg Ser Leu His Ala Ser Leu Leu Val Val Thr Leu Asn
      225      230      235      240
Pro Lys His Cys His Pro Ser Ser Arg Lys Arg Arg Ala Ala Ile Ser
      245      250      255
Val Pro Lys Gly Phe Cys Arg Asn Phe Cys His Arg His Gln Leu Phe
      260      265      270
Ile Asn Phe Gln Asp Leu Gly Trp His Lys Trp Val Ile Ala Pro Lys
      275      280      285
Gly Phe Met Ala Asn Tyr Cys His Gly Glu Cys Pro Phe Ser Met Thr
      290      295      300
Thr Tyr Leu Asn Ser Ser Asn Tyr Ala Phe Met Gln Ala Leu Met His
      305      310      315      320
Met Ala Asp Pro Lys Val Pro Lys Ala Val Cys Val Pro Thr Lys Leu
      325      330      335
Ser Pro Ile Ser Met Leu Tyr Gln Asp Ser Asp Lys Asn Val Ile Leu
      340      345      350
Arg His Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Gly
      355      360      365

```

```

<210> 33
<211> 1224
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (37)..(1128)

```

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<400> 33
ggagctctcc ccggtctgac agccactcca gagggc atg ctt cgt ttc ttg cca 54
Met Leu Arg Phe Leu Pro
1      5

gat ttg gct ttc agc ttc ctg tta att ctg gct ttg ggc cag gca gtc 102
Asp Leu Ala Phe Ser Phe Leu Leu Ile Leu Ala Leu Gly Gln Ala Val
10      15      20

```

## 701049\_sequence\_listing.txt

caa	ttt	caa	gaa	tat	gtc	ttt	ctc	caa	ttt	ctg	ggc	tta	gat	aag	gcg	150
Gln	Phe	Gln	Glu	Tyr	Val	Phe	Leu	Gln	Phe	Leu	Gly	Leu	Asp	Lys	Ala	
		25					30					35				
cct	tca	ccc	cag	aag	ttc	caa	cct	gtg	cct	tat	atc	ttg	aag	aaa	att	198
Pro	Ser	Pro	Gln	Lys	Phe	Gln	Pro	Val	Pro	Tyr	Ile	Leu	Lys	Lys	Ile	
	40					45					50					
ttc	cag	gat	cgc	gag	gca	gca	gcg	acc	act	ggg	gtc	tcc	cga	gac	tta	246
Phe	Gln	Asp	Arg	Glu	Ala	Ala	Ala	Thr	Thr	Gly	Val	Ser	Arg	Asp	Leu	
55					60					65					70	
tgc	tac	gta	aag	gag	ctg	ggc	gtc	cgc	ggg	aat	gta	ctt	cgc	ttt	ctc	294
Cys	Tyr	Val	Lys	Glu	Leu	Gly	Val	Arg	Gly	Asn	Val	Leu	Arg	Phe	Leu	
				75					80					85		
cca	gac	caa	ggt	ttc	ttt	ctt	tac	cca	aag	aaa	att	tcc	caa	gct	tcc	342
Pro	Asp	Gln	Gly	Phe	Phe	Leu	Tyr	Pro	Lys	Lys	Ile	Ser	Gln	Ala	Ser	
			90					95					100			
tcc	tgc	ctg	cag	aag	ctc	ctc	tac	ttt	aac	ctg	tct	gcc	atc	aaa	gaa	390
Ser	Cys	Leu	Gln	Lys	Leu	Leu	Tyr	Phe	Asn	Leu	Ser	Ala	Ile	Lys	Glu	
		105					110					115				
agg	gaa	cag	ttg	aca	ttg	gcc	cag	ctg	ggc	ctg	gac	ttg	ggg	ccc	aat	438
Arg	Glu	Gln	Leu	Thr	Leu	Ala	Gln	Leu	Gly	Leu	Asp	Leu	Gly	Pro	Asn	
	120					125					130					
tct	tac	tat	aac	ctg	gga	cca	gag	ctg	gaa	ctg	gct	ctg	ttc	ctg	gtt	486
Ser	Tyr	Tyr	Asn	Leu	Gly	Pro	Glu	Leu	Glu	Leu	Ala	Leu	Phe	Leu	Val	
135					140					145					150	
cag	gag	cct	cat	gtg	tgg	ggc	cag	acc	acc	cct	aag	cca	ggt	aaa	atg	534
Gln	Glu	Pro	His	Val	Trp	Gly	Gln	Thr	Thr	Pro	Lys	Pro	Gly	Lys	Met	
				155					160					165		
ttt	gtg	ttg	cgg	tca	gtc	cca	tgg	cca	caa	ggt	gct	gtt	cac	ttc	aac	582
Phe	Val	Leu	Arg	Ser	Val	Pro	Trp	Pro	Gln	Gly	Ala	Val	His	Phe	Asn	
			170				175						180			
ctg	ctg	gat	gta	gct	aag	gat	tgg	aat	gac	aac	ccc	cgg	aaa	aat	ttc	630
Leu	Leu	Asp	Val	Ala	Lys	Asp	Trp	Asn	Asp	Asn	Pro	Arg	Lys	Asn	Phe	
		185					190					195				
ggg	tta	ttc	ctg	gag	ata	ctg	gtc	aaa	gaa	gat	aga	gac	tca	ggg	gtg	678
Gly	Leu	Phe	Leu	Glu	Ile	Leu	Val	Lys	Glu	Asp	Arg	Asp	Ser	Gly	Val	
	200					205					210					
aat	ttt	cag	cct	gaa	gac	acc	tgt	gcc	aga	cta	aga	tgc	tcc	ctt	cat	726
Asn	Phe	Gln	Pro	Glu	Asp	Thr	Cys	Ala	Arg	Leu	Arg	Cys	Ser	Leu	His	
215					220					225					230	
gct	tcc	ctg	ctg	gtg	gtg	act	ctc	aac	cct	gat	cag	tgc	cac	cct	tct	774
Ala	Ser	Leu	Leu	Val	Val	Thr	Leu	Asn	Pro	Asp	Gln	Cys	His	Pro	Ser	
				235					240					245		
cgg	aaa	agg	aga	gca	gcc	atc	cct	gtc	ccc	aag	ctt	tct	tgt	aag	aac	822
Arg	Lys	Arg	Arg	Ala	Ala	Ile	Pro	Val	Pro	Lys	Leu	Ser	Cys	Lys	Asn	
			250					255					260			
ctc	tgc	cac	cgt	cac	cag	cta	ttc	att	aac	ttc	cgg	gac	ctg	ggt	tgg	870
Leu	Cys	His	Arg	His	Gln	Leu	Phe	Ile	Asn	Phe	Arg	Asp	Leu	Gly	Trp	
		265					270					275				

## 701049\_sequence\_listing.txt

```

cac aag tgg atc att gcc ccc aag ggg ttc atg gca aat tac tgc cat 918
His Lys Trp Ile Ile Ala Pro Lys Gly Phe Met Ala Asn Tyr Cys His
280 285 290

gga gag tgt ccc ttc tca ctg acc atc tct ctc aac agc tcc aat tat 966
Gly Glu Cys Pro Phe Ser Leu Thr Ile Ser Leu Asn Ser Ser Asn Tyr
295 300 305 310

gct ttc atg caa gcc ctg atg cat gcc gtt gac cca gag atc ccc cag 1014
Ala Phe Met Gln Ala Leu Met His Ala Val Asp Pro Glu Ile Pro Gln
315 320 325

gct gtg tgt atc ccc acc aag ctg tct ccc att tcc atg ctc tac cag 1062
Ala Val Cys Ile Pro Thr Lys Leu Ser Pro Ile Ser Met Leu Tyr Gln
330 335 340

gac aat aat gac aat gtc att cta cga cat tat gaa gac atg gta gtc 1110
Asp Asn Asn Asp Asn Val Ile Leu Arg His Tyr Glu Asp Met Val Val
345 350 355

gat gaa tgt ggg tgt ggg taggatgtca gaaatgggaa tagaaggagt 1158
Asp Glu Cys Gly Cys Gly

gttcttaggg taaatctttt aataaaaacta cctatctggg ttatgaccac ttagatcgaa 1218
atgtca 1224

```

```

<210> 34
<211> 364
<212> PRT
<213> Homo sapiens

```

```

<400> 34
Met Leu Arg Phe Leu Pro Asp Leu Ala Phe Ser Phe Leu Leu Ile Leu
1 5 10 15

Ala Leu Gly Gln Ala Val Gln Phe Gln Glu Tyr Val Phe Leu Gln Phe
20 25 30

Leu Gly Leu Asp Lys Ala Pro Ser Pro Gln Lys Phe Gln Pro Val Pro
35 40 45

Tyr Ile Leu Lys Lys Ile Phe Gln Asp Arg Glu Ala Ala Ala Thr Thr
50 55 60

Gly Val Ser Arg Asp Leu Cys Tyr Val Lys Glu Leu Gly Val Arg Gly
65 70 75 80

Asn Val Leu Arg Phe Leu Pro Asp Gln Gly Phe Phe Leu Tyr Pro Lys
85 90 95

Lys Ile Ser Gln Ala Ser Ser Cys Leu Gln Lys Leu Leu Tyr Phe Asn
100 105 110

Leu Ser Ala Ile Lys Glu Arg Glu Gln Leu Thr Leu Ala Gln Leu Gly
115 120 125

Leu Asp Leu Gly Pro Asn Ser Tyr Tyr Asn Leu Gly Pro Glu Leu Glu
130 135 140

```

701049\_sequence\_listing.txt

Leu Ala Leu Phe Leu Val Gln Glu Pro His Val Trp Gly Gln Thr Thr  
145 150 155 160  
Pro Lys Pro Gly Lys Met Phe Val Leu Arg Ser Val Pro Trp Pro Gln  
165 170 175  
Gly Ala Val His Phe Asn Leu Leu Asp Val Ala Lys Asp Trp Asn Asp  
180 185 190  
Asn Pro Arg Lys Asn Phe Gly Leu Phe Leu Glu Ile Leu Val Lys Glu  
195 200 205  
Asp Arg Asp Ser Gly Val Asn Phe Gln Pro Glu Asp Thr Cys Ala Arg  
210 215 220  
Leu Arg Cys Ser Leu His Ala Ser Leu Leu Val Val Thr Leu Asn Pro  
225 230 235 240  
Asp Gln Cys His Pro Ser Arg Lys Arg Arg Ala Ala Ile Pro Val Pro  
245 250 255  
Lys Leu Ser Cys Lys Asn Leu Cys His Arg His Gln Leu Phe Ile Asn  
260 265 270  
Phe Arg Asp Leu Gly Trp His Lys Trp Ile Ile Ala Pro Lys Gly Phe  
275 280 285  
Met Ala Asn Tyr Cys His Gly Glu Cys Pro Phe Ser Leu Thr Ile Ser  
290 295 300  
Leu Asn Ser Ser Asn Tyr Ala Phe Met Gln Ala Leu Met His Ala Val  
305 310 315 320  
Asp Pro Glu Ile Pro Gln Ala Val Cys Ile Pro Thr Lys Leu Ser Pro  
325 330 335  
Ile Ser Met Leu Tyr Gln Asp Asn Asn Asp Asn Val Ile Leu Arg His  
340 345 350  
Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Gly  
355 360

<210> 35  
<211> 1248  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (32)..(1003)

<400> 35  
agtggatccc ccgggctgca ggaattccgg g atg gat cct cga acc tgg cta 52  
Met Asp Pro Arg Thr Trp Leu  
1 5  
agc ttc caa ggg cct cca ggt ggg cct gga atc gga cca ggc tca gag 100  
Ser Phe Gln Gly Pro Pro Gly Gly Pro Gly Ile Gly Pro Gly Ser Glu  
10 15 20  
gta ttg ggg atc tcc cca tgt ccg ccc gca tac gag ttc tgc gga ggg 148  
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## 701049\_sequence\_listing.txt

Val	Leu	Gly	Ile	Ser	Pro	Cys	Pro	Pro	Ala	Tyr	Glu	Phe	Cys	Gly	Gly	
	25					30					35					
atg Met 40	gca Ala	tac Tyr	tgt Cys	gga Gly	cct Pro 45	cag Gln	ggt Val	ggt Gly	ctg Leu	ggc Gly 50	cta Leu	gtc Val	ccc Pro	caa Gln	gtt Val 55	196
ggc Gly	gtg Val	gag Glu	act Thr	ttg Leu 60	cag Gln	cct Pro	gag Glu	ggc Gly	cag Gln 65	gca Ala	gga Gly	gca Ala	cga Arg	gtg Val 70	gaa Glu	244
agc Ser	aac Asn	tca Ser	gag Glu 75	gga Gly	acc Thr	tcc Ser	tct Ser	gag Glu 80	ccc Pro	tgt Cys	gcc Ala	gac Asp	cgc Arg 85	ccc Pro	aat Asn	292
gcc Ala	gtg Val	aag Lys 90	ttg Leu	gag Glu	aag Lys	gtg Val	gaa Glu 95	cca Pro	act Thr	ccc Pro	gag Glu 100	gag Glu 100	tcc Ser	cag Gln	gac Asp	340
atg Met 105	aaa Lys	gcc Ala	ctg Leu	cag Gln	aag Lys	gag Glu 110	cta Leu	gaa Glu	cag Gln	ttt Phe	gcc Ala 115	aag Lys	ctg Leu	ctg Leu	aag Lys	388
cag Gln 120	aag Lys	agg Arg	atc Ile	acc Thr	ttg Leu 125	ggg Gly	tac Tyr	acc Thr	cag Gln	gcc Ala 130	gac Asp	gtg Val	ggg Gly	ctc Leu 135	acc Thr 135	436
ctg Leu	ggc Gly	gtt Val	ctc Leu	ttt Phe 140	gga Gly	aag Lys	gtg Val	ttc Phe	agc Ser 145	cag Gln	acc Thr	acc Thr	atc Ile	tgt Cys 150	cgc Arg	484
ttc Phe	gag Glu	gcc Ala	ttg Leu 155	cag Gln	ctc Leu	agc Ser	ctt Leu	aag Lys 160	aac Asn	atg Met	tgt Cys	aag Lys	ctg Leu 165	cgg Arg	ccc Pro	532
ctg Leu	ctg Leu	gag Glu 170	aag Lys	tgg Trp	gtg Val	gag Glu	gaa Glu 175	gcc Ala	gac Asp	aac Asn	aat Asn	gag Glu 180	aac Asn	ctt Leu	cag Gln	580
gag Glu 185	ata Ile	tgc Cys	aaa Lys	tcg Ser	gag Glu	acc Thr 190	ctg Leu	gtg Val	cag Gln	gcc Ala	cgg Arg 195	aag Lys	aga Arg	aag Lys	cga Arg	628
act Thr 200	agc Ser	att Ile	gag Glu	aac Asn	cgt Arg 205	gtg Val	agg Arg	tgg Trp	agt Ser	ctg Leu 210	gag Glu	acc Thr	atg Met	ttt Phe	ctg Leu 215	676
aag Lys	tgc Cys	ccg Pro	aag Lys	ccc Pro 220	tcc Ser	cta Leu	cag Gln	cag Gln	atc Ile 225	act Thr	cac His	atc Ile	gcc Ala	aat Asn 230	cag Gln	724
ctt Leu	ggg Gly	cta Leu	gag Glu 235	aag Lys	gat Asp	gtg Val	gtt Val	cga Arg 240	gta Val	tgg Trp	ttc Phe	tgt Cys	aac Asn 245	cgg Arg	cgc Arg	772
cag Gln	aag Lys	ggc Gly 250	aaa Lys	aga Arg	tca Ser	agt Ser	att Ile 255	gag Glu	tat Tyr	tcc Ser	caa Gln	cga Arg 260	gaa Glu	gag Glu	tat Tyr	820
gag Glu	gct Ala 265	aca Thr	ggg Gly	aca Thr	cct Pro	ttc Phe 270	cca Pro	ggg Gly	ggg Gly	gct Ala	gta Val 275	tcc Ser	ttt Phe	cct Pro	ctg Leu	868



## 701049\_sequence\_listing.txt

```

ccc cca ggt ccc cac ttt ggc acc cca ggc tat gga agc ccc cac ttc 916
Pro Pro Gly Pro His Phe Gly Thr Pro Gly Tyr Gly Ser Pro His Phe
280 285 290 295

acc aca ctc tac tca gtc cct ttt cct gag ggc gag gcc ttt ccc tct 964
Thr Thr Leu Tyr Ser Val Pro Phe Pro Glu Gly Glu Ala Phe Pro Ser
300 305 310

gtt ccc gtc act gct ctg ggc tct ccc atg cat tca aac tgaggcacca 1013
Val Pro Val Thr Ala Leu Gly Ser Pro Met His Ser Asn
315 320

gccctccctg gggatgctgt gagccaaggc aaggaggagta gacaagagaa cctggagctt 1073
tggggttaaa ttcttttact gaggagggat taaaagcaca acaggggtgg ggggtgggat 1133
ggggaaagaa gctcagtgat gctgttgatc aggagcctgg cctgtctgtc actcatcatt 1193
ttgttcttaa ataaagactg ggacacacag taaaaaaaaa aaaaaaaaaac tcgag 1248

<210> 36
<211> 324
<212> PRT
<213> Mus musculus

<400> 36
Met Asp Pro Arg Thr Trp Leu Ser Phe Gln Gly Pro Pro Gly Gly Pro
1 5 10 15
Gly Ile Gly Pro Gly Ser Glu Val Leu Gly Ile Ser Pro Cys Pro Pro
20 25 30
Ala Tyr Glu Phe Cys Gly Gly Met Ala Tyr Cys Gly Pro Gln Val Gly
35 40 45
Leu Gly Leu Val Pro Gln Val Gly Val Glu Thr Leu Gln Pro Glu Gly
50 55 60
Gln Ala Gly Ala Arg Val Glu Ser Asn Ser Glu Gly Thr Ser Ser Glu
65 70 75 80
Pro Cys Ala Asp Arg Pro Asn Ala Val Lys Leu Glu Lys Val Glu Pro
85 90 95
Thr Pro Glu Glu Ser Gln Asp Met Lys Ala Leu Gln Lys Glu Leu Glu
100 105 110
Gln Phe Ala Lys Leu Leu Lys Gln Lys Arg Ile Thr Leu Gly Tyr Thr
115 120 125
Gln Ala Asp Val Gly Leu Thr Leu Gly Val Leu Phe Gly Lys Val Phe
130 135 140
Ser Gln Thr Thr Ile Cys Arg Phe Glu Ala Leu Gln Leu Ser Leu Lys
145 150 155 160
Asn Met Cys Lys Leu Arg Pro Leu Leu Glu Lys Trp Val Glu Glu Ala
165 170 175
Asp Asn Asn Glu Asn Leu Gln Glu Ile Cys Lys Ser Glu Thr Leu Val
180 185 190

```

## 701049\_sequence\_listing.txt

Gln Ala Arg Lys Arg Lys Arg Thr Ser Ile Glu Asn Arg Val Arg Trp  
 195 200 205  
 Ser Leu Glu Thr Met Phe Leu Lys Cys Pro Lys Pro Ser Leu Gln Gln  
 210 215 220  
 Ile Thr His Ile Ala Asn Gln Leu Gly Leu Glu Lys Asp Val Val Arg  
 225 230 235 240  
 Val Trp Phe Cys Asn Arg Arg Gln Lys Gly Lys Arg Ser Ser Ile Glu  
 245 250 255  
 Tyr Ser Gln Arg Glu Glu Tyr Glu Ala Thr Gly Thr Pro Phe Pro Gly  
 260 265 270  
 Gly Ala Val Ser Phe Pro Leu Pro Pro Gly Pro His Phe Gly Thr Pro  
 275 280 285  
 Gly Tyr Gly Ser Pro His Phe Thr Thr Leu Tyr Ser Val Pro Phe Pro  
 290 295 300  
 Glu Gly Glu Ala Phe Pro Ser Val Pro Val Thr Ala Leu Gly Ser Pro  
 305 310 315 320  
 Met His Ser Asn

<210> 37  
 <211> 1371  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (43)..(1122)

<400> 37  
 ctcatttcac caggcccccg gcttggggcg ccttccttcc cc atg gcg gga cac 54  
 Met Ala Gly His  
 1  
 ctg gct tcg gat ttc gcc ttc tcg ccc cct cca ggt ggt gga ggt gat 102  
 Leu Ala Ser Asp Phe Ala Phe Ser Pro Pro Pro Gly Gly Gly Gly Asp  
 5 10 15 20  
 ggg cca ggg ggg ccg gag ccg ggc tgg gtt gat cct cgg acc tgg cta 150  
 Gly Pro Gly Gly Pro Glu Pro Gly Trp Val Asp Pro Arg Thr Trp Leu  
 25 30 35  
 agc ttc caa ggc cct cct gga ggg cca gga atc ggg ccg ggg gtt ggg 198  
 Ser Phe Gln Gly Pro Pro Gly Gly Pro Gly Ile Gly Pro Gly Val Gly  
 40 45 50  
 cca ggc tct gag gtg tgg ggg att ccc cca tgc ccc ccg ccg tat gag 246  
 Pro Gly Ser Glu Val Trp Gly Ile Pro Pro Cys Pro Pro Pro Tyr Glu  
 55 60 65  
 ttc tgt ggg ggg atg gcg tac tgt ggg ccc cag gtt gga gtg ggg cta 294  
 Phe Cys Gly Gly Met Ala Tyr Cys Gly Pro Gln Val Gly Val Gly Leu  
 70 75 80

## 701049\_sequence\_listing.txt

gtg Val 85	ccc Pro	caa Gln	ggc Gly	ggc Gly	ttg Leu 90	gag Glu	acc Thr	tct Ser	cag Gln	cct Pro 95	gag Glu	ggc Gly	gaa Glu	gca Ala	gga Gly 100	342
gtc Val	ggg Gly	gtg Val	gag Glu	agc Ser 105	aac Asn	tcc Ser	gat Asp	ggg Gly	gcc Ala 110	tcc Ser	ccg Pro	gag Glu	ccc Pro	tgc Cys 115	acc Thr	390
gtc Val	acc Thr	cct Pro	ggt Gly 120	gcc Ala	gtg Val	aag Lys	ctg Leu	gag Glu 125	aag Lys	gag Glu	aag Lys	ctg Leu	gag Glu 130	caa Gln	aac Asn	438
ccg Pro	gag Glu	gag Glu 135	tcc Ser	cag Gln	gac Asp	atc Ile	aaa Lys 140	gct Ala	ctg Leu	cag Gln	aaa Lys	gaa Glu 145	ctc Leu	gag Glu	caa Gln	486
ttt Phe	gcc Ala 150	aag Lys	ctc Leu	ctg Leu	aag Lys	cag Gln 155	aag Lys	agg Arg	atc Ile	acc Thr	ctg Leu 160	gga Gly	tat Tyr	aca Thr	cag Gln	534
gcc Ala 165	gat Asp	gtg Val	ggg Gly	ctc Leu	acc Thr 170	ctg Leu	ggg Gly	gtt Val	cta Leu	ttt Phe 175	ggg Gly	aag Lys	gta Val	ttc Phe	agc Ser 180	582
caa Gln	acg Thr	acc Thr	atc Ile	tgc Cys 185	cgc Arg	ttt Phe	gag Glu	gct Ala	ctg Leu 190	cag Gln	ctt Leu	agc Ser	ttc Phe	aag Lys 195	aac Asn	630
atg Met	tgt Cys	aag Lys	ctg Leu 200	cgg Arg	ccc Pro	ttg Leu	ctg Leu	cag Gln 205	aag Lys	tgg Trp	gtg Val	gag Glu	gaa Glu 210	gct Ala	gac Asp	678
aac Asn	aat Asn	gaa Glu 215	aat Asn	ctt Leu	cag Gln	gag Glu	ata Ile 220	tgc Cys	aaa Lys	gca Ala	gaa Glu	acc Thr 225	ctc Leu	gtg Val	cag Gln	726
gcc Ala	cga Arg 230	aag Lys	aga Arg	aag Lys	cga Arg	acc Thr 235	agt Ser	atc Ile	gag Glu	aac Asn	cga Arg 240	gtg Val	aga Arg	ggc Gly	aac Asn	774
ctg Leu 245	gag Glu	aat Asn	ttg Leu	ttc Phe	ctg Leu 250	cag Gln	tgc Cys	ccg Pro	aaa Lys	ccc Pro 255	aca Thr	ctg Leu	cag Gln	cag Gln	atc Ile 260	822
agc Ser	cac His	atc Ile	gcc Ala	cag Gln 265	cag Gln	ctt Leu	ggg Gly	ctc Leu	gag Glu 270	aag Lys	gat Asp	gtg Val	gtc Val	cga Arg 275	gtg Val	870
tgg Trp	ttc Phe	tgt Cys	aac Asn 280	cgg Arg	cgc Arg	cag Gln	aag Lys	ggc Gly 285	aag Lys	cga Arg	tca Ser	agc Ser	agc Ser 290	gac Asp	tat Tyr	918
gca Ala	caa Gln	cga Arg 295	gag Glu	gat Asp	ttt Phe	gag Glu	gct Ala 300	gct Ala	ggg Gly	tct Ser	cct Pro	ttc Phe 305	tca Ser	ggg Gly	gga Gly	966
cca Pro	gtg Val 310	tcc Ser	ttt Phe	cct Pro	ctg Leu	gcc Ala 315	cca Pro	ggg Gly	ccc Pro	cat His	ttt Phe 320	ggt Gly	acc Thr	cca Pro	ggc Gly	1014
tat Tyr 325	ggg Gly	agc Ser	cct Pro	cac His	ttc Phe 330	act Thr	gca Ala	ctg Leu	tac Tyr	tcc Ser 335	tcg Ser	gtc Val	cct Pro	ttc Phe	cct Pro 340	1062

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gag ggg gaa gcc ttt ccc cct gtc tct gtc acc act ctg ggc tct ccc 1110  
Glu Gly Glu Ala Phe Pro Pro Val Ser Val Thr Thr Leu Gly Ser Pro  
345 350 355

atg cat tca aac tgaggtgcct gcccttctag gaatggggga cagggggagg 1162  
Met His Ser Asn  
360

ggaggagcta gggaaagaaa acctggagtt tgtgccaggg tttttggatt aagttcttca 1222  
ttcactaagg aaggaattgg gaacacaaag ggtggggggca ggggagtttg gggcaactgg 1282  
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20 25 30  
Arg Thr Trp Leu Ser Phe Gln Gly Pro Pro Gly Gly Pro Gly Ile Gly  
35 40 45  
Pro Gly Val Gly Pro Gly Ser Glu Val Trp Gly Ile Pro Pro Cys Pro  
50 55 60  
Pro Pro Tyr Glu Phe Cys Gly Gly Met Ala Tyr Cys Gly Pro Gln Val  
65 70 75 80  
Gly Val Gly Leu Val Pro Gln Gly Gly Leu Glu Thr Ser Gln Pro Glu  
85 90 95  
Gly Glu Ala Gly Val Gly Val Glu Ser Asn Ser Asp Gly Ala Ser Pro  
100 105 110  
Glu Pro Cys Thr Val Thr Pro Gly Ala Val Lys Leu Glu Lys Glu Lys  
115 120 125  
Leu Glu Gln Asn Pro Glu Glu Ser Gln Asp Ile Lys Ala Leu Gln Lys  
130 135 140  
Glu Leu Glu Gln Phe Ala Lys Leu Leu Lys Gln Lys Arg Ile Thr Leu  
145 150 155 160  
Gly Tyr Thr Gln Ala Asp Val Gly Leu Thr Leu Gly Val Leu Phe Gly  
165 170 175  
Lys Val Phe Ser Gln Thr Thr Ile Cys Arg Phe Glu Ala Leu Gln Leu  
180 185 190  
Ser Phe Lys Asn Met Cys Lys Leu Arg Pro Leu Leu Gln Lys Trp Val  
195 200 205

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Glu Glu Ala Asp Asn Asn Glu Asn Leu Gln Glu Ile Cys Lys Ala Glu  
 210 215 220  
 Thr Leu Val Gln Ala Arg Lys Arg Lys Arg Thr Ser Ile Glu Asn Arg  
 225 230 235 240  
 Val Arg Gly Asn Leu Glu Asn Leu Phe Leu Gln Cys Pro Lys Pro Thr  
 245 250 255  
 Leu Gln Gln Ile Ser His Ile Ala Gln Gln Leu Gly Leu Glu Lys Asp  
 260 265 270  
 Val Val Arg Val Trp Phe Cys Asn Arg Arg Gln Lys Gly Lys Arg Ser  
 275 280 285  
 Ser Ser Asp Tyr Ala Gln Arg Glu Asp Phe Glu Ala Ala Gly Ser Pro  
 290 295 300  
 Phe Ser Gly Gly Pro Val Ser Phe Pro Leu Ala Pro Gly Pro His Phe  
 305 310 315 320  
 Gly Thr Pro Gly Tyr Gly Ser Pro His Phe Thr Ala Leu Tyr Ser Ser  
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 Leu Gly Ser Pro Met His Ser Asn  
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701049\_sequence\_listing.txt

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